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OM protein - protein search, using sw model

Run on: May 18, 2004, 12:08:12 ; Search time 48 Seconds
(without alignments)
2104.352 Million cell updates/sec

Title: US-10-049-569-2

Perfect score: 1858
Sequence: 1 MGFEALLAGLLVMVLAVAL.....ASTHNGSVTDNSCLQOHT 363

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 1145568 seqs, 278261457 residues

Total number of hits satisfying chosen parameters: 1145568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1858	100.0	363	9	US-09-736-131-2
2	1858	100.0	363	10	US-09-782-974C-186
3	1858	100.0	363	12	US-10-206-915-590
4	1858	100.0	363	12	US-10-199-670-590
5	1858	100.0	363	12	US-10-201-858-590
6	1858	100.0	363	12	US-10-205-890-590
7	1858	100.0	363	12	US-10-208-024-590
8	1858	100.0	363	12	US-10-201-853-590
9	1858	100.0	363	12	US-10-174-581-590
10	1858	100.0	363	12	US-10-176-483-590
11	1858	100.0	363	12	US-10-176-749-590
12	1858	100.0	363	12	US-10-176-914-590
13	1858	100.0	363	12	US-10-176-915-590
14	1858	100.0	363	12	US-10-176-484-590
15	1858	100.0	363	12	US-10-180-550-590

16	1858	100.0	363	12	US-10-183-014-590	Sequence 590, App
17	1858	100.0	363	12	US-10-187-738-590	Sequence 590, App
18	1858	100.0	363	12	US-10-187-740-590	Sequence 590, App
19	1858	100.0	363	12	US-10-187-883-590	Sequence 590, App
20	1858	100.0	363	12	US-10-194-363-590	Sequence 590, App
21	1858	100.0	363	12	US-10-194-460-590	Sequence 590, App
22	1858	100.0	363	12	US-10-194-463-590	Sequence 590, App
23	1858	100.0	363	12	US-10-194-484-590	Sequence 590, App
24	1858	100.0	363	12	US-10-195-884-590	Sequence 590, App
25	1858	100.0	363	12	US-10-195-896-590	Sequence 590, App
26	1858	100.0	363	12	US-10-196-744-590	Sequence 590, App
27	1858	100.0	363	12	US-10-196-755-590	Sequence 590, App
28	1858	100.0	363	12	US-10-197-704-590	Sequence 590, App
29	1858	100.0	363	12	US-10-197-710-590	Sequence 590, App
30	1858	100.0	363	12	US-10-198-758-590	Sequence 590, App
31	1858	100.0	363	12	US-10-198-766-590	Sequence 590, App
32	1858	100.0	363	12	US-10-199-304-590	Sequence 590, App
33	1858	100.0	363	12	US-10-199-309-590	Sequence 590, App
34	1858	100.0	363	12	US-10-199-313-590	Sequence 590, App
35	1858	100.0	363	12	US-10-199-456-590	Sequence 590, App
36	1858	100.0	363	12	US-10-201-329-590	Sequence 590, App
37	1858	100.0	363	12	US-10-202-412-590	Sequence 590, App
38	1858	100.0	363	12	US-10-206-919-590	Sequence 590, App
39	1858	100.0	363	12	US-10-206-922-590	Sequence 590, App
40	1858	100.0	363	12	US-10-206-924-590	Sequence 590, App
41	1858	100.0	363	12	US-10-207-914-590	Sequence 590, App
42	1858	100.0	363	12	US-10-207-921-590	Sequence 590, App
43	1858	100.0	363	12	US-10-207-922-590	Sequence 590, App
44	1858	100.0	363	12	US-10-207-922-590	Sequence 590, App
45	1858	100.0	363	12	US-10-207-922-590	Sequence 590, App

ALIGNMENTS

RESULT 1

US-09-736-131-2
; Sequence 2, Application US/09736131
; Patent No. US20020019347A1
; GENERAL INFORMATION:
; APPLICANT: GUEGLER et al.
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL000738
; CURRENT APPLICATION NUMBER: US/09/736,131
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 60/219,449
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 363
; TYPE: PRT
; ORGANISM: Human
US-09-736-131-2

Query Match 100.0%; Score 1858; DB 9; Length 363;
Best Local Similarity 100.0%; Pred. No. 2.48-169;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGFEALLAGLLVMVLAVALSNALVLLCCAYSABLRTRAGVLLVNLGLHLLAALDM 60
Db 1 MGFEALLAGLLVMVLAVALSNALVLLCCAYSABLRTRAGVLLVNLGLHLLAALDM 60
QY 61 PTLTGLWVRGTPSAGACQVIGFLDTFLASNAALSVAAASADQWLAVGFFLYAGRLRP 120
Db 61 PTLTGLWVRGTPSAGACQVIGFLDTFLASNAALSVAAASADQWLAVGFFLYAGRLRP 120
QY 121 RVAGLLGCWQSLAFSGAALGCSWLGYSSAFASCSLRPPPRPFAATLHVG 180
Db 121 RVAGLLGCWQSLAFSGAALGCSWLGYSSAFASCSLRPPPRPFAATLHVG 180

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QY 181 FVLPLAVLCITSLQVHRVARHRCQMDTVMKALALLADLHPSVRQRCCLIOQKRRHRAT 240
Db 181 FVLPLAVLCITSLQVHRVARHRCQMDTVMKALALLADLHPSVRQRCCLIOQKRRHRAT 240
QY 241 RKIGIAIAFLICFAPYVMTRELAEVLPFTVNAQWGLSKCLITYSKAVADPFTYSLLRRP 300
Db 241 RKIGIAIAFLICFAPYVMTRELAEVLPFTVNAQWGLSKCLITYSKAVADPFTYSLLRRP 300
QY 301 FRQVLGVMVHRLKRTPRPASTHSDSLDVAGVMHQLLKTTPRPASTHNGSVDTENDSCLO 360
Db 301 FRQVLGVMVHRLKRTPRPASTHSDSLDVAGVMHQLLKTTPRPASTHNGSVDTENDSCLO 360
QY 361 QTH 363
Db 361 QTH 363

RESULT 2
US-09-782-974C-186
; Sequence 186, Application US/09782974C
; Publication No. US20030082534A1
; GENERAL INFORMATION:
; APPLICANT: Vogel, Gabriel
; APPLICANT: Lind, Peter
; APPLICANT: Wood, Linda S.
; APPLICANT: Parodi, Luis A.
; TITLE OF INVENTION: No. US20030082534A1el G Protein Coupled Receptor
; FILE REFERENCE: 41USPRM311
; CURRENT APPLICATION NUMBER: US/09/782,974C
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 60/165,838
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 09/714,449
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 60/198,568
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 60/166,071
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/166,678
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: 60/173,396
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/184,129
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/185,421
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/185,554
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/186,530
; PRIOR FILING DATE: 2000-03-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 186
; LENGTH: 363
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-782-974C-186

Query Match 100.0%; Score 1858; DB 10; Length 363;
Best Local Similarity 100.0%; Pred. No. 2.4e-169;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGPEALLAGLVVAVALLSNALVLLCCAYSAELTRASGVLLVNLGLHLLAALDM 60
Db 1 MGPEALLAGLVVAVALLSNALVLLCCAYSAELTRASGVLLVNLGLHLLAALDM 60
QY 61 PFTLLGVMGRGTSAPGACOVIGFLDTFFLASNAALSVAAALSDQWLAVGFFPLRYAGRLRP 120
Db 61 PFTLLGVMGRGTSAPGACOVIGFLDTFFLASNAALSVAAALSDQWLAVGFFPLRYAGRLRP 120
QY 121 RYAGLLGCWAGSLAFSGAALGCSWLGYSAPASCSLRLPPEPRPFAATLHVG 180
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Db 121 RYAGLLGCWAGSLAFSGAALGCSWLGYSAPASCSLRLPPEPRPFAATLHVG 180
QY 181 FVLPLAVLCITSLQVHRVARHRCQMDTVMKALALLADLHPSVRQRCCLIOQKRRHRAT 240
Db 181 FVLPLAVLCITSLQVHRVARHRCQMDTVMKALALLADLHPSVRQRCCLIOQKRRHRAT 240
QY 241 RKIGIAIAFLICFAPYVMTRELAEVLPFTVNAQWGLSKCLITYSKAVADPFTYSLLRRP 300
Db 241 RKIGIAIAFLICFAPYVMTRELAEVLPFTVNAQWGLSKCLITYSKAVADPFTYSLLRRP 300
QY 301 FRQVLGVMVHRLKRTPRPASTHSDSLDVAGVMHQLLKTTPRPASTHNGSVDTENDSCLO 360
Db 301 FRQVLGVMVHRLKRTPRPASTHSDSLDVAGVMHQLLKTTPRPASTHNGSVDTENDSCLO 360
QY 361 QTH 363
Db 361 QTH 363

RESULT 3
US-10-206-915-590
; Sequence 590, Application US/10206915
; Publication No. US20040029221A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P343ORIC513
; CURRENT APPLICATION NUMBER: US/10/206,915
; CURRENT FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 590
; LENGTH: 363
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-206-915-590

Query Match 100.0%; Score 1858; DB 12; Length 363;
Best Local Similarity 100.0%; Pred. No. 2.4e-169;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGPEALLAGLVVAVALLSNALVLLCCAYSAELTRASGVLLVNLGLHLLAALDM 60
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; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION DATA REMOVED - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 590
; LENGTH: 363
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-201-858-590

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Best Local Similarity 100.0%; Pred. No. 2.4e-169; Indels 0; Gaps 0;
Matches 363; Conservative 0; Mismatches 0;

QY   1 MGPGALLAGLLVMVLAVALLSNALVLCCAYSaelrtrasgvllvnslgHLLLAAALDM 60
    |||                               ||||                             ||||
DB   1 MGPGALLAGLLVMVLAVALLSNALVLCCAYSaelrtrasgvllvnslgHLLLAAALDM 60

QY   61 PTTLGVNRGTPSPAGCAQCIGFDLTFASNAALSVAALSADQLAVGPFLRYAglRLP 120
    |||                               ||||                             ||||
DB   61 PTTLGVNRGTPSPAGCAQCIGFDLTFASNAALSVAALSADQLAVGPFLRYAglRLP 120

QY   121 RYAGLLGCWQSIAFSGALGCSWLGYSAFAfscSLRlPPePERPRFAFTATLHAVG 180
    |||                               ||||                             ||||
DB   121 RYAGLLGCWQSIAFSGALGCSWLGYSAFAfscSLRlPPePERPRFAFTATLHAVG 180

QY   181 FYPLAVLCtLSLOHVRRHCQRMDVTWKAlalladlhPSVRqCLLIQQKrrHRat 240
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DB   181 FYPLAVLCtLSLOHVRRHCQRMDVTWKAlalladlhPSVRqCLLIQQKrrHRat 240

QY   241 RKIGIAtIFLICFPAYMTrlAEtlVPvTNaQGILSKclTySkavAdPfTYSlLRrp 300
    |||                               ||||                             ||||
DB   241 RKIGIAtIFLICFPAYMTrlAEtlVPvTNaQGILSKclTySkavAdPfTYSlLRrp 300

QY   301 FRQVLAgmVhRLlkrtPrPaSThdSSLDVGAmVHQllkrtPrPaStngSVdTeNDSClQ 360
    |||                               ||||                             ||||
DB   301 FRQVLAgmVhRLlkrtPrPaSThdSSLDVGAmVHQllkrtPrPaStngSVdTeNDSClQ 360

QY   361 QTH 363
    |||
DB   361 QTH 363


RESULT 6
US-10-205-890-590
; Sequence 590, Application US/10205890
; Publication No. US20040048334A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R/C519
; CURRENT APPLICATION NUMBER: US/10/205,890
; CURRENT FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18

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FILE REFERENCE: P3430R1C538
 CURRENT APPLICATION NUMBER: US/10/208,024
 CURRENT FILING DATE: 2002-07-29
 PRIOR APPLICATION NUMBER: 10/052586
 PRIOR FILING DATE: 2002-01-15
 PRIOR APPLICATION NUMBER: 60/059263
 PRIOR FILING DATE: 1997-09-18
 PRIOR APPLICATION NUMBER: 60/059266
 PRIOR FILING DATE: 1997-09-18
 PRIOR APPLICATION NUMBER: 60/062250
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/063120
 PRIOR FILING DATE: 1997-10-24
 PRIOR APPLICATION NUMBER: 60/063121
 PRIOR FILING DATE: 1997-10-24
 PRIOR APPLICATION NUMBER: 60/063486
 PRIOR FILING DATE: 1997-10-21
 PRIOR APPLICATION NUMBER: 60/063540
 PRIOR FILING DATE: 1997-10-28
 PRIOR APPLICATION NUMBER: 60/063541
 PRIOR FILING DATE: 1997-10-28
 PRIOR APPLICATION NUMBER: 60/063544
 PRIOR FILING DATE: 1997-10-28
 Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 612
 SEQ ID NO 590
 LENGTH: 363
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-10-208-024-590

Query Match 100.0%; Score 1858; DB 12; Length 363;
 Best Local Similarity 100.0%; Pred. No. 2.4e-169; Indels 0; Gaps 0;
 Matches 363; Conservative 0; Mismatches 0;

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Db	1	MGPEALLAGLLVWVLAVALLSNALVLLCCAYSAELRTRASGVLLVNLISLGHLLAALDM	60
QY	61	PFTLLGVMRGRTSPAGACQVIGFDTFLASNAALSVAALSADQWLAVGPFPLRYAGRLRP	120
Db	61	PFTLLGVMRGRTSPAGACQVIGFDTFLASNAALSVAALSADQWLAVGPFPLRYAGRLRP	120
QY	121	RYAGLLGCWAGQSIAFSGAALGCSWLGYSAPASCSLRLPPEPRPFAAFTATLHVG	180
Db	121	RYAGLLGCWAGQSIAFSGAALGCSWLGYSAPASCSLRLPPEPRPFAAFTATLHVG	180
QY	181	FVLPLAVLCLTSLQVHRVAREHCQMDVTVMKALALLADLHPSVQRCLIQKRRHRAT	240
Db	181	FVLPLAVLCLTSLQVHRVAREHCQMDVTVMKALALLADLHPSVQRCLIQKRRHRAT	240
QY	241	RKIGIAIATFLICFAPYVMTLAEVLPFTVNAQWGLSKCLTYSKAVADPFTYSLRRP	300
Db	241	RKIGIAIATFLICFAPYVMTLAEVLPFTVNAQWGLSKCLTYSKAVADPFTYSLRRP	300
QY	301	PROVLGVMVHLLKRTPRPASTHSSLDVAGMVHQLLKRTPRPASTHNGSVDTENDSCIQ	360
Db	301	PROVLGVMVHLLKRTPRPASTHSSLDVAGMVHQLLKRTPRPASTHNGSVDTENDSCIQ	360
QY	361	QTH 363	
Db	361	QTH 363	

RESULT 8
 US-10-201-853-590
 Sequence 590, Application US/10201853
 Publication No. US20040053358A1
 GENERAL INFORMATION:
 APPLICANT: Baker, Kevin P.
 APPLICANT: Chen, Jian
 APPLICANT: Desnoyers, Luc
 APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Pan, James
 APPLICANT: Smith, Victoria
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 FILE REFERENCE: P3430R1C465
 CURRENT APPLICATION NUMBER: US/10/201,853
 CURRENT FILING DATE: 2002-07-23
 PRIOR APPLICATION NUMBER: 10/052586
 PRIOR FILING DATE: 2002-01-15
 PRIOR APPLICATION NUMBER: 60/059263
 PRIOR FILING DATE: 1997-09-18
 PRIOR APPLICATION NUMBER: 60/059266
 PRIOR FILING DATE: 1997-09-18
 PRIOR APPLICATION NUMBER: 60/062250
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/063120
 PRIOR FILING DATE: 1997-10-24
 PRIOR APPLICATION NUMBER: 60/063121
 PRIOR FILING DATE: 1997-10-24
 PRIOR APPLICATION NUMBER: 60/063486
 PRIOR FILING DATE: 1997-10-21
 PRIOR APPLICATION NUMBER: 60/063540
 PRIOR FILING DATE: 1997-10-28
 PRIOR APPLICATION NUMBER: 60/063541
 PRIOR FILING DATE: 1997-10-28
 PRIOR APPLICATION NUMBER: 60/063544
 PRIOR FILING DATE: 1997-10-28
 Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 612
 SEQ ID NO 590
 LENGTH: 363
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-10-201-853-590

Query Match 100.0%; Score 1858; DB 12; Length 363;
 Best Local Similarity 100.0%; Pred. No. 2.4e-169; Indels 0; Gaps 0;
 Matches 363; Conservative 0; Mismatches 0;

QY	1	MGPEALLAGLLVWVLAVALLSNALVLLCCAYSAELRTRASGVLLVNLISLGHLLAALDM	60
Db	1	MGPEALLAGLLVWVLAVALLSNALVLLCCAYSAELRTRASGVLLVNLISLGHLLAALDM	60
QY	61	PFTLLGVMRGRTSPAGACQVIGFDTFLASNAALSVAALSADQWLAVGPFPLRYAGRLRP	120
Db	61	PFTLLGVMRGRTSPAGACQVIGFDTFLASNAALSVAALSADQWLAVGPFPLRYAGRLRP	120
QY	121	RYAGLLGCWAGQSIAFSGAALGCSWLGYSAPASCSLRLPPEPRPFAAFTATLHVG	180
Db	121	RYAGLLGCWAGQSIAFSGAALGCSWLGYSAPASCSLRLPPEPRPFAAFTATLHVG	180
QY	181	FVLPLAVLCLTSLQVHRVAREHCQMDVTVMKALALLADLHPSVQRCLIQKRRHRAT	240
Db	181	FVLPLAVLCLTSLQVHRVAREHCQMDVTVMKALALLADLHPSVQRCLIQKRRHRAT	240
QY	241	RKIGIAIATFLICFAPYVMTLAEVLPFTVNAQWGLSKCLTYSKAVADPFTYSLRRP	300
Db	241	RKIGIAIATFLICFAPYVMTLAEVLPFTVNAQWGLSKCLTYSKAVADPFTYSLRRP	300
QY	301	PROVLGVMVHLLKRTPRPASTHSSLDVAGMVHQLLKRTPRPASTHNGSVDTENDSCIQ	360
Db	301	PROVLGVMVHLLKRTPRPASTHSSLDVAGMVHQLLKRTPRPASTHNGSVDTENDSCIQ	360
QY	361	QTH 363	
Db	361	QTH 363	

RESULT 9
US-10-174-581-590
; Sequence 590 Application US/10174581
; Publication No. US20030017540A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430RIC41
; CURRENT APPLICATION NUMBER: US/10/174,581
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063564
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063734
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/063870
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066120
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/066466
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/066772
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/069335
; PRIOR FILING DATE: 1997-12-11
; PRIOR APPLICATION NUMBER: 60/069425
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: 60/069870
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/068017
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/078886
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078939
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079664
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079786
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/080107
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080194
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080327
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080333
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/081049
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081070
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081195
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081838
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082568
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082569
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082704
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082797
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/083495
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083496
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083499
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083559
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/084366
; PRIOR FILING DATE: 1998-05-05
; PRIOR APPLICATION NUMBER: 60/084414
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084639
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084640
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084643
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/086023
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/086392
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/086486
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087098
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087208
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759

181 FVLPLAVLCITSLQVHVRVARRHCOQMDTVMKALALLADLHPSVRQCLIQCKERRHRAT 24
 181 FVLPLAVLCITSLQVHVRVARRHCOQMDTVMKALALLADLHPSVRQCLIQCKERRHRAT 24
 241 RKIGIATATFLICFAPVYVMTLRAELVPEFVTVNAQWGILSKCLITYSKAVADPFTYSLLRP 30
 241 RKIGIATATFLICFAPVYVMTLRAELVPEFVTVNAQWGILSKCLITYSKAVADPFTYSLLRP 30
 301 PROVLAVMVRHLLKRTPRPASTHDSLLDVAGMVHQLKRTPRPASTHNGSVDTENDSCLO 36
 301 PROVLAVMVRHLLKRTPRPASTHDSLLDVAGMVHQLKRTPRPASTHNGSVDTENDSCLO 36
 361 QTH 363
 361 QTH 363
 RESULT 10
 US-10-176-483-590
 ; Sequence 590, Application US/10176483
 ; Publication No. US20030017541A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Pan, James
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; TITLE OF INVENTION: ACIDS ENCODING THE SAME
 ; FILE REFERENCE: P3430RIC88
 ; CURRENT APPLICATION NUMBER: US/10/176,483
 ; CURRENT FILING DATE: 2002-06-20
 ; Prior application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 612
 ; SEQ ID NO 590
 ; LENGTH: 363
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-176-483-590
 Query Match 100.0%; Score 1858; DB 12; Length 363;
 Best Local Similarity 100.0%; Pred. No. 2.4e-169;
 Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0
 QY 1 MGPGALLAGLLVMVLAVALLSNALVLLCCAYSAAELTRASGVLLVNLSLGHLILAALDM 60
 DB 1 MGPGALLAGLLVMVLAVALLSNALVLLCCAYSAAELTRASGVLLVNLSLGHLILAALDM 60
 QY 61 PFTLLGVMRGRTSPAGCAQVIGFLDTFLASNALSVAAALSADQWLAVGFLRYAGRLRP 120
 DB 61 PFTLLGVMRGRTSPAGCAQVIGFLDTFLASNALSVAAALSADQWLAVGFLRYAGRLRP 120
 QY 121 RYAGLLGCWAGSLAFSGAALGCSWLGYSASFASCSRLRPPPERPFAAFTATLHVG 180
 DB 121 RYAGLLGCWAGSLAFSGAALGCSWLGYSASFASCSRLRPPPERPFAAFTATLHVG 180
 QY 181 FVLPLAVLCITSLQVHVRVARRHCOQMDTVMKALALLADLHPSVRQCLIQCKERRHRAT 240
 DB 181 FVLPLAVLCITSLQVHVRVARRHCOQMDTVMKALALLADLHPSVRQCLIQCKERRHRAT 240
 QY 241 RKIGIATATFLICFAPVYVMTLRAELVPEFVTVNAQWGILSKCLITYSKAVADPFTYSLLRP 300
 DB 241 RKIGIATATFLICFAPVYVMTLRAELVPEFVTVNAQWGILSKCLITYSKAVADPFTYSLLRP 300
 QY 301 PROVLAVMVRHLLKRTPRPASTHDSLLDVAGMVHQLKRTPRPASTHNGSVDTENDSCLO 360
 DB 301 PROVLAVMVRHLLKRTPRPASTHDSLLDVAGMVHQLKRTPRPASTHNGSVDTENDSCLO 360

QY 361 QTH 363
 Db 361 QTH 363

RESULT 11

US-10-176-749-590

; Sequence 590, Application US/10176749

; Publication No. US20030017542A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P3430R1C76

; CURRENT APPLICATION NUMBER: US/10/176,749

; CURRENT FILING DATE: 2002-06-20

; Prior application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 590

; LENGTH: 363

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-176-749-590

Query Match 100.0%; Score 1858; DB 12; Length 363;

Best Local Similarity 100.0%; Pred. No. 2.4e-169;

Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGPEGALLAGLLVMVLAVALLSNALVLLCCAYSABLRTRASGVLLVNLISLGHLLAALDM 60

Db 1 MGPEGALLAGLLVMVLAVALLSNALVLLCCAYSABLRTRASGVLLVNLISLGHLLAALDM 60

QY 61 PFTLLGVMRGRTSPAGACQVIGFDTFLASNAALSVAAALSADQWLAVGFFPLRYAGRLRP 120

Db 61 PFTLLGVMRGRTSPAGACQVIGFDTFLASNAALSVAAALSADQWLAVGFFPLRYAGRLRP 120

QY 121 RYAGLLGCWAGCSLAFSGAALGCSWLGYSFASCSRLRPPPEPRPFAAFTATLHVG 180

Db 121 RYAGLLGCWAGCSLAFSGAALGCSWLGYSFASCSRLRPPPEPRPFAAFTATLHVG 180

QY 181 FVLPLAVLCLTSLQVHRVARRHCQMDVTVMKALALLADLHPSVRQRCIIQKRRHRAT 240

Db 181 FVLPLAVLCLTSLQVHRVARRHCQMDVTVMKALALLADLHPSVRQRCIIQKRRHRAT 240

QY 241 RKIGIAIATFLICFAPYVMTRLAELVPFVTVNAQNGILSKCLITYSKAVADPFTYSLLRP 300

Db 241 RKIGIAIATFLICFAPYVMTRLAELVPFVTVNAQNGILSKCLITYSKAVADPFTYSLLRP 300

QY 301 FROVLAGMVRHLIKRTPRPASTDSSLDVAGMVHQLKTRTPASTHNGSVDTENDSCIQ 360

Db 301 FROVLAGMVRHLIKRTPRPASTDSSLDVAGMVHQLKTRTPASTHNGSVDTENDSCIQ 360

QY 361 QTH 363

Db 361 QTH 363

RESULT 12

US-10-176-914-590

; Sequence 590, Application US/10176914

; Publication No. US20030017543A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Pan, James
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3430R1C83
 ; CURRENT APPLICATION NUMBER: US/10/176,914
 ; CURRENT FILING DATE: 2002-06-20
 ; Prior application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 612
 ; SEQ ID NO 590
 ; LENGTH: 363
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-176-914-590

Query Match 100.0%; Score 1858; DB 12; Length 363;

Best Local Similarity 100.0%; Pred. No. 2.4e-169;

Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGPEGALLAGLLVMVLAVALLSNALVLLCCAYSABLRTRASGVLLVNLISLGHLLAALDM 60

Db 1 MGPEGALLAGLLVMVLAVALLSNALVLLCCAYSABLRTRASGVLLVNLISLGHLLAALDM 60

QY 61 PFTLLGVMRGRTSPAGACQVIGFDTFLASNAALSVAAALSADQWLAVGFFPLRYAGRLRP 120

Db 61 PFTLLGVMRGRTSPAGACQVIGFDTFLASNAALSVAAALSADQWLAVGFFPLRYAGRLRP 120

QY 121 RYAGLLGCWAGCSLAFSGAALGCSWLGYSFASCSRLRPPPEPRPFAAFTATLHVG 180

Db 121 RYAGLLGCWAGCSLAFSGAALGCSWLGYSFASCSRLRPPPEPRPFAAFTATLHVG 180

QY 181 FVLPLAVLCLTSLQVHRVARRHCQMDVTVMKALALLADLHPSVRQRCIIQKRRHRAT 240

Db 181 FVLPLAVLCLTSLQVHRVARRHCQMDVTVMKALALLADLHPSVRQRCIIQKRRHRAT 240

QY 241 RKIGIAIATFLICFAPYVMTRLAELVPFVTVNAQNGILSKCLITYSKAVADPFTYSLLRP 300

Db 241 RKIGIAIATFLICFAPYVMTRLAELVPFVTVNAQNGILSKCLITYSKAVADPFTYSLLRP 300

QY 301 FROVLAGMVRHLIKRTPRPASTDSSLDVAGMVHQLKTRTPASTHNGSVDTENDSCIQ 360

Db 301 FROVLAGMVRHLIKRTPRPASTDSSLDVAGMVHQLKTRTPASTHNGSVDTENDSCIQ 360

QY 361 QTH 363

Db 361 QTH 363

RESULT 13

US-10-176-915-590

; Sequence 590, Application US/10176915

; Publication No. US20030017544A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

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/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE OF INVENTION: ACIDS ENCODING THE SAME
/ FILE REFERENCE: P3430R1C110
/ CURRENT APPLICATION NUMBER: US/10/176,915
/ CURRENT FILING DATE: 2002-06-21
/ Prior application removed - See File Wrapper or Palm
/ NUMBER OF SEQ ID NOS: 612
/ SEQ ID NO 590
/ LENGTH: 363
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-176-915-590

Query Match      100.0%; Score 1858; DB 12; Length 363;
Best Local Similarity 100.0%; Pred. No. 2.4e-169;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGPGEALLAGLLVMVLAVALLSNALVLLCCAYSAELRTRASGVLLVNLGLHLLAALDM 60
DB 1 MGPGEALLAGLLVMVLAVALLSNALVLLCCAYSAELRTRASGVLLVNLGLHLLAALDM 60
QY 61 PPTLLGVNRGRTSPAGACQVIGFLDTFLASNAALSVAAALSADQWLAVGFFPLRYAGRLRP 120
DB 61 PPTLLGVNRGRTSPAGACQVIGFLDTFLASNAALSVAAALSADQWLAVGFFPLRYAGRLRP 120
QY 121 RVAGLLGCAGWGQSLAFSGAALGCSWLGYSFAFASCSLRLPEPERPFAAFTATLHVG 180
DB 121 RVAGLLGCAGWGQSLAFSGAALGCSWLGYSFAFASCSLRLPEPERPFAAFTATLHVG 180
QY 181 FVLPLAVLCLSQVHRVARRHCQMDVTVMKALALLADLHPSVRCCLIOQKRRHRAT 240
DB 181 FVLPLAVLCLSQVHRVARRHCQMDVTVMKALALLADLHPSVRCCLIOQKRRHRAT 240
QY 241 RKIGIAIATFLICFAPYVMTRLAELVPFVTVNAQWGLSKCLTYSKAVADPFTYSLLRP 300
DB 241 RKIGIAIATFLICFAPYVMTRLAELVPFVTVNAQWGLSKCLTYSKAVADPFTYSLLRP 300
QY 301 FRQVLGVMVHRLKRTPRPASTHSSLDVAGMVHQLKRTPRPASTHNGSVDTENDSCLQ 360
DB 301 FRQVLGVMVHRLKRTPRPASTHSSLDVAGMVHQLKRTPRPASTHNGSVDTENDSCLQ 360
QY 361 QTH 363
DB 361 QTH 363

RESULT 14
US-10-176-484-590
/ Sequence 590, Application US/10176484
/ Publication No. US2003059876A9
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Chen, Jian
/ APPLICANT: Deenoyers, Luc
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Pan, James
/ APPLICANT: Smith, Victoria
/ APPLICANT: Watanabe, Colin K.
/ APPLICANT: Wood, William I.
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE OF INVENTION: ACIDS ENCODING THE SAME
/ FILE REFERENCE: P3430R1C64
/ CURRENT APPLICATION NUMBER: US/10/176,484
/ CURRENT FILING DATE: 2002-06-20
/ Prior application removed - See File Wrapper or Palm
/ NUMBER OF SEQ ID NOS: 612
/ SEQ ID NO 590
/ LENGTH: 363
/ TYPE: PRT
/ ORGANISM: Homo Sapien

Query Match      100.0%; Score 1858; DB 12; Length 363;
Best Local Similarity 100.0%; Pred. No. 2.4e-169;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGPGEALLAGLLVMVLAVALLSNALVLLCCAYSAELRTRASGVLLVNLGLHLLAALDM 60
DB 1 MGPGEALLAGLLVMVLAVALLSNALVLLCCAYSAELRTRASGVLLVNLGLHLLAALDM 60
QY 61 PPTLLGVNRGRTSPAGACQVIGFLDTFLASNAALSVAAALSADQWLAVGFFPLRYAGRLRP 120
DB 61 PPTLLGVNRGRTSPAGACQVIGFLDTFLASNAALSVAAALSADQWLAVGFFPLRYAGRLRP 120
QY 121 RVAGLLGCAGWGQSLAFSGAALGCSWLGYSFAFASCSLRLPEPERPFAAFTATLHVG 180
DB 121 RVAGLLGCAGWGQSLAFSGAALGCSWLGYSFAFASCSLRLPEPERPFAAFTATLHVG 180
QY 181 FVLPLAVLCLSQVHRVARRHCQMDVTVMKALALLADLHPSVRCCLIOQKRRHRAT 240
DB 181 FVLPLAVLCLSQVHRVARRHCQMDVTVMKALALLADLHPSVRCCLIOQKRRHRAT 240
QY 241 RKIGIAIATFLICFAPYVMTRLAELVPFVTVNAQWGLSKCLTYSKAVADPFTYSLLRP 300
DB 241 RKIGIAIATFLICFAPYVMTRLAELVPFVTVNAQWGLSKCLTYSKAVADPFTYSLLRP 300
QY 301 FRQVLGVMVHRLKRTPRPASTHSSLDVAGMVHQLKRTPRPASTHNGSVDTENDSCLQ 360
DB 301 FRQVLGVMVHRLKRTPRPASTHSSLDVAGMVHQLKRTPRPASTHNGSVDTENDSCLQ 360
QY 361 QTH 363
DB 361 QTH 363

RESULT 15
US-10-180-550-590
/ Sequence 590, Application US/10180550
/ Publication No. US2003006440A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Chen, Jian
/ APPLICANT: Deenoyers, Luc
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Pan, James
/ APPLICANT: Smith, Victoria
/ APPLICANT: Watanabe, Colin K.
/ APPLICANT: Wood, William I.
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE OF INVENTION: ACIDS ENCODING THE SAME
/ FILE REFERENCE: P3430R1C149
/ CURRENT APPLICATION NUMBER: US/10/180,550
/ CURRENT FILING DATE: 2002-06-25
/ Prior application removed - See File Wrapper or Palm
/ NUMBER OF SEQ ID NOS: 612
/ SEQ ID NO 590
/ LENGTH: 363
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-180-550-590

Query Match      100.0%; Score 1858; DB 12; Length 363;
Best Local Similarity 100.0%; Pred. No. 2.4e-169;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGPGEALLAGLLVMVLAVALLSNALVLLCCAYSAELRTRASGVLLVNLGLHLLAALDM 60
DB 1 MGPGEALLAGLLVMVLAVALLSNALVLLCCAYSAELRTRASGVLLVNLGLHLLAALDM 60
QY 61 PPTLLGVNRGRTSPAGACQVIGFLDTFLASNAALSVAAALSADQWLAVGFFPLRYAGRLRP 120
DB 61 PPTLLGVNRGRTSPAGACQVIGFLDTFLASNAALSVAAALSADQWLAVGFFPLRYAGRLRP 120
QY 121 RVAGLLGCAGWGQSLAFSGAALGCSWLGYSFAFASCSLRLPEPERPFAAFTATLHVG 180
DB 121 RVAGLLGCAGWGQSLAFSGAALGCSWLGYSFAFASCSLRLPEPERPFAAFTATLHVG 180
QY 181 FVLPLAVLCLSQVHRVARRHCQMDVTVMKALALLADLHPSVRCCLIOQKRRHRAT 240
DB 181 FVLPLAVLCLSQVHRVARRHCQMDVTVMKALALLADLHPSVRCCLIOQKRRHRAT 240
QY 241 RKIGIAIATFLICFAPYVMTRLAELVPFVTVNAQWGLSKCLTYSKAVADPFTYSLLRP 300
DB 241 RKIGIAIATFLICFAPYVMTRLAELVPFVTVNAQWGLSKCLTYSKAVADPFTYSLLRP 300
QY 301 FRQVLGVMVHRLKRTPRPASTHSSLDVAGMVHQLKRTPRPASTHNGSVDTENDSCLQ 360
DB 301 FRQVLGVMVHRLKRTPRPASTHSSLDVAGMVHQLKRTPRPASTHNGSVDTENDSCLQ 360
QY 361 QTH 363
DB 361 QTH 363
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Tue May 18 14:14:52 2004

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Qy	121	RYAGLLIGCANGOSLAFSGALGCSWLGYSAPASCSRLRPPPEPRPFAAFTATLHVG	180
Db	121	RYAGLLIGCANGOSLAFSGALGCSWLGYSAPASCSRLRPPPEPRPFAAFTATLHVG	180
Qy	181	FVLPFLAVLCLTSLQVHRVARRHCOEMDTVTMKALALADLHPSVORCLIQOKRRHRAT	240
Db	181	FVLPFLAVLCLTSLQVHRVARRHCOEMDTVTMKALALADLHPSVORCLIQOKRRHRAT	240
Qy	241	RKIGIAIATFLICFAPYVMTLAEVFPVTVNAQWGLSKCLTYSKAVADPETYSLLRP	300
Db	241	RKIGIAIATFLICFAPYVMTLAEVFPVTVNAQWGLSKCLTYSKAVADPETYSLLRP	300
Qy	301	PROVLAGVHRLKRTPRPASTHDSLDVAGMVHQLLKRTPRPASTHNGSVDTENDSCLQ	360
Db	301	PROVLAGVHRLKRTPRPASTHDSLDVAGMVHQLLKRTPRPASTHNGSVDTENDSCLQ	360
Qy	361	QTH	363
Db	361	QTH	363

Search completed: May 18, 2004, 12:14:05
Job time : 50 secs

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OM protein - protein search, using sw model

Run on: May 18, 2004, 12:04:02 ; Search time 20 seconds
(without alignments)
1745.876 Million cell updates/sec

Title: US-10-049-569-2

Perfect score: 1858

Sequence: 1 MGPEALLAGLVNVLAVALL.....ASTHNGSVDTENDSCLQPTH 363

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78:*

1: Pirl1.*

2: Pirl2.*

3: Pirl3.*

4: Pirl4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	248	13.3	437	2 157942	5-hydroxytryptamin
2	244.5	13.2	440	JC5520	serotonin receptor
3	243.5	13.1	388	2 JN0605	somatostatin recep
4	239	12.9	436	2 JN0591	serotonin receptor
5	232.5	12.5	359	2 JC4120	histamine H2 recep
6	231.5	12.5	364	2 JN0753	somatostatin recep
7	231	12.4	363	2 157955	somatostatin recep
8	230.5	12.4	408	1 QRHUBE	beta-3-adrenergic
9	230.5	12.4	414	1 QRHUB3	beta-3-adrenergic
10	229.5	12.4	418	2 G02953	beta-3-adrenergic
11	228.5	12.3	363	2 157940	somatostatin recep
12	228.5	12.3	391	2 A41795	somatostatin recep
13	228.5	12.3	391	2 C41795	somatostatin recep
14	228.5	12.3	391	2 A39297	somatostatin recep
15	228.5	12.3	477	1 DYHDS5	dopamine receptor
16	228	12.3	387	2 JC5949	galanin receptor 2
17	228	12.3	475	2 A41271	dopamine receptor
18	226.5	12.2	420	2 T25689	hypothetical prote
19	224	12.1	457	2 151660	dopamine H2 recep
20	223.5	12.0	359	2 A39008	histamine D1 recep
21	223	12.0	369	2 B41795	somatostatin recep
22	223	12.0	445	2 A48881	serotonin receptor
23	222.5	12.0	384	2 A47249	brain-specific som
24	222	11.9	368	2 A45291	somatostatin recep
25	222	11.9	449	2 A47519	serotonin receptor
26	222	11.9	459	2 A56849	dopamine receptor
27	221	11.9	369	2 JC2083	somatostatin recep
28	220	11.8	359	2 JH0449	histamine H2 recep
29	220	11.8	370	2 148231	serotonin receptor

30	220	11.8	477	2 S71323	alpha-1A adrenergic
31	219	11.8	564	2 A38271	serotonin receptor
32	216	11.6	397	1 DYHDA4	dopamine receptor
33	216	11.6	448	2 S36402	serotonin receptor
34	216	11.6	560	2 A38731	alpha-1A adrenergic
35	215.5	11.6	358	2 JQ1278	histamine H2 recep
36	215	11.6	387	2 S55550	5-HT4S receptor -
37	215	11.6	451	2 I51659	dopamine D1A recep
38	214.5	11.5	444	2 C55986	dopamine receptor
39	214	11.5	418	2 A46226	somatostatin recep
40	213.5	11.5	400	2 S32804	beta-3-adrenergic
41	213	11.5	369	2 D41795	somatostatin recep
42	212.5	11.4	363	2 I50475	dopamine D1 recep
43	212	11.4	406	2 S55549	serotonin 4 recep
44	212	11.4	428	2 S30508	probable G protein
45	212	11.4	487	1 DYRTD1	dopamine receptor

ALIGNMENTS

RESULT 1

157942

S-hydroxytryptamine receptor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999

C:Accession: 157942

R:Monism, F.J.

Mol. Pharmacol. 43, 320-327, 1993

A:Title: Cloning and expression of a novel serotonin receptor with high affinity for tri-

A:Reference number: 157942; PMID:7680751

A:Accession: 157942

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-437 <RES>

A:Cross-references: GB:I03202; NID:G294507; PIDN:AAA40618.1; PID:G294508

C:Superfamily: vertebrate rhodopsin

Query Match 13.3%; Score 248; DB 2; Length 437;

Best Local Similarity 25.3%; Pred. No. 3.3e-13;

Matches 93; Conservative 63; Mismatches 166; Indels 46; Gaps 12;

QY	2	GPGEA-----LLAGLVNVLAVALLSNVALLCCAYSAELRTFASGVLLVNLGLHL	53
DB	16	GPGEPPAPGGSGWVAALCVIVLTAAANSLIVLICITQPAVRNT--SNFFVLSFTSDL	73
QY	54	LLAALDMPFTLLGVMGRTPSPAGCAQVIGFDTFTLASNAALSVAALSADOMLAVGFPLR	113
DB	74	MVGLVMPAPMLNLYGRWVLAGLCLLTAFDVMCCSASILNLCISLDLYLLILSPLR	133
QY	114	YAGEL-RPRYAGLLLCANGQSIA-----FSGALGCSWLYGSSAFASCSLRLPPEPRR	168
DB	134	YKURMTAPRALITLG-AW--SLAALASFLPLLGHWEHLGKART-----PAGQCR	181
QY	169	FAA---FTATLHAGVFLPLAVLCLTSLQVHRVARHRCQMDTDT-----MKALALIA	218
DB	182	LLASLPVLVASGVTFPLFSGAICFTYCRILLAAKQAVQVASLTGTGAQALETLQVPR	241
QY	219	DLPSVR-----QRCLTQOKRRRRATRKIGIALTFILCFAPYVMTRLAELVFFVTVNAQ	274
DB	242	TPRPGMESADSRRLATYKSKAKASLTIGLIGMFFVFWLFFVFWNTAQAQVCCDCLISPL	301
QY	275	WGILSKCLTYKAVADPFYTLRRRFRFQVLAGWVHRLKRTFRPASTHSSDLSLVAGMVH	334
DB	302	FDVLT-WLGYCNSMTNPIYPLFMRFKRALG----RFLHASTVPRSTGQCLPLHVDLS	356
QY	335	QLLKRTPR	342
DB	357	QRCTRQ	364

RESULT 2

JC5520

serotonin receptor 6 - human
N:Alternate names: 5-hydroxytryptamine receptor 6 (5-HT6)
C:Species: Homo sapiens (man)
C:Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 05-Nov-1999
C:Accession: J05520
R:Kohen, R.; Metcalf, M.A.; Khan, N.; Druck, T.; Huebner, K.; Lachowicz, J.E.; Meltzer, J. Neurochem. 66, 47-56, 1996
A:Title: Cloning, characterization, and chromosomal localization of a human 5-HT 6 sero
A:Reference number: J05520; MUID:96102917; PMID:8522988
A:Accession: J05520
A:Molecule type: mRNA
A:Residues: 1-440 <KOH>
A:Cross-references: GB:I41147; NID:G1162923; PIDN:AAA92622.1; PID:G1162924
A:Experimental source: brain
C:Comment: This protein shows high affinity for several therapeutically important antide
C:Genetics:
A:Gene: HTR6
A:Map position: 1p35-36
A:Introns: 238/3; 291/3
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transme
F:28-51/Domain: transmembrane #status predicted <TM1>
F:65-88/Domain: transmembrane #status predicted <TM2>
F:100-123/Domain: transmembrane #status predicted <TM3>
F:143-166/Domain: transmembrane #status predicted <TM4>
F:186-208/Domain: transmembrane #status predicted <TM5>
F:266-289/Domain: transmembrane #status predicted <TM6>
F:298-321/Domain: transmembrane #status predicted <TM7>
F:10/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 13.2%; Score 244.5; DB 2; Length 440;
Best Local Similarity 26.1%; Pred. No. 6.5e-13;
Matches 102; Conservative 64; Mismatches 164; Indels 61; Gaps 17;
QY 2 GP-----GELLAGLLVMVLAVALLSNALVL-LCCAYSLELTRASGVLLVNLGLHLL 55
DB 18 GPPSAPGSGVAAALCVIALTAANSLIALICTQPALRNT--SNFFLVSLFTSLDW 75
QY 56 AALDMPTLLGVNRGRTSPAGCAQVIGFDTFLASNAALSAALSAADOMLAVGFLRYA 115
DB 76 GLVMPFAMNLALYGRVLAARGLCLLWTAFDVMCCSASILNCLISLDYLLLSPLRYK 135
QY 116 GLRPR-RIAGLLGCAGQSLA-----FSGAALGCSWLGYSSAFASCSLRLLPEPRPFA 170
DB 136 LRMTPLRALVLG-AW--SLAALASFLPLLLGWHELGHAR-----PPVPGQCRLL 183
QY 171 A---FTATLHAGVFLPLAVLCILTSQVHRVARRHCQMDIVT-----MKALALLADL 220
DB 184 ASLPFVLVAGSLTFLEPSGAICFTYCRILLAAKQAVQASLTTCWASQASSETLOVPETP 243
QY 221 HPSVR-----ORCLQKRRHRATRKIGIAIATFLICFAPYVMTLAEVLVFTVNAQWG 276
DB 244 RGVESADSRRLATKHSRKALKASLTGILLGNFFVTWLPFFVANIQAQVDCISPGGLFD 303
QY 277 ILSKCLTYKXAVADPPFTYSLRPPFQVLAGVMVHLL--KRTF--RPASTHDSLLDVA-- 330
DB 304 VLT-WLGYCNSWNPIIPLFWDFKALG-----RELPCPRCPRQASLASPSLRTSHS 358
QY 331 ----GMVHQLKKTTPRPAHSTNGSVTENDS 357
DB 359 GPRFGSLQQVLPFLPLFP-----DSDS 382
RESULT 3
JN0605
somatostatin receptor 4 - human
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 20-Jun-2000
C:Accession: JN0605; JN0762; A47457
R:Xu, Y.; Song, J.; Bruno, J.F.; Berelowitz, M.
Biochem. Biophys. Res. Commun. 193, 648-652, 1993
A:Title: Molecular cloning and sequencing of a human somatostatin receptor, hsstr4.
A:Reference number: JN0605; MUID:93290656; PMID:8512564

A:Accession: JN0605
A:Molecule type: DNA
A:Residues: 1-388 <XUY>
A:Cross-references: GB:I14856; NID:G292499; PIDN:AAA36623.1; PID:G292500
R:Yamada, Y.; Kagimoto, S.; Kubota, A.; Yasuda, K.; Someya, Y.; Ihara, Y.; Li
Biochem. Biophys. Res. Commun. 195, 844-852, 1993
A:Title: Cloning, functional expression and pharmacological characterization of a fourth
A:Reference number: JN0762; MUID:93384611; PMID:8373420
A:Accession: JN0762
A:Molecule type: DNA
A:Residues: 1-388 <YAM>
A:Cross-references: GB:D16826; NID:G693907; PIDN:BA04106.1; PID:G693908
R:Rohrer, L.; Raulf, F.; Bruns, C.; Buettner, R.; Hofstaedter, F.; Schulte, R.
Proc. Natl. Acad. Sci. U.S.A. 90, 4196-4200, 1993
A:Title: Cloning and characterization of a fourth human somatostatin receptor.
A:Reference number: A47457; MUID:93240256; PMID:8483934
A:Accession: A47457
A:Molecule type: DNA
A:Residues: 1-82, 'T', '84-364, 'K', '366-388 <ROH>
A:Cross-references: GB:L07833; NID:G307429; PIDN:AAA60565.1; PID:G307430
A:Note: sequence extracted from NCBI backbone (NCBIN:130856, NCBIPI:130858)
C:Comment: This protein mediates the diverse actions of the tetradecapide somatostatin.
C:Genetics:
A:Gene: GDB:SSTR4
A:Cross-references: GDB:202662; OMIM:182454
A:Map position: 20p11.2-20p11.2
C:Superfamily: G protein-coupled receptor; glycoprotein; hormone receptor; lipoprotein; photo
C:Keywords: G protein-coupled receptor; glycoprotein; hormone receptor; lipoprotein; photo
F:47-73/Domain: transmembrane #status predicted <TM1>
F:84-109/Domain: transmembrane #status predicted <TM2>
F:121-142/Domain: transmembrane #status predicted <TM3>
F:162-184/Domain: transmembrane #status predicted <TM4>
F:208-238/Domain: transmembrane #status predicted <TM5>
F:257-284/Domain: transmembrane #status predicted <TM6>
F:291-314/Domain: transmembrane #status predicted <TM7>
F:24/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:119-198/Disulfide bonds: #status predicted
F:161,253/Binding site: phosphate (Ser) (covalent) (by CAMP-dependent kinase) #status pre
F:327/Binding site: palmitate (Cys) (covalent) #status predicted
Query Match 13.1%; Score 243.5; DB 2; Length 388;
Best Local Similarity 25.5%; Pred. No. 6.9e-13;
Matches 84; Conservative 55; Mismatches 124; Indels 67; Gaps 10;
QY 2 GPGEALLAGLL-----VMVLAVALLSNALVLLCCAYSLELTRASGVLLVNLGLHLL 55
DB 38 GPGDARAAGVIAQCIYALVCLVGLVGNALVIFVILRYAKMKT-ATNIIYLLNLADEL 96
QY 56 AALDMPTLLGVNRGRTSPAGCAQVIGFDTFLASNAALSAALSAADOMLAVGFLRYA 115
DB 97 -WLSVFPFVASSAALRHHWPFSGVLCRAVLSVDGLNFTSVFCLTVLSVDYVAVVHPDRAA 155
QY 116 GLRPRYAGLLIGCAGQSL-----AFSGAALGCS--WLGYSSAFASCSLR 159
DB 156 TYRRESVAKLNLGVWLASLLVTLPIAFADTRPARGQAVACNLQW----- 202
QY 160 LPPEPRPFAFTATLHAGVFLPLAVLCILTSQVHRVARRHCQMDYTMKALLAD 219
DB 203 ----PHPAWSAVFVYVYTFLLGFLPLVLAIGL-----CYLLVSGKRAVALRAG 246
QY 220 LHPVSQRCLIQKRRHRATRKIGIAIATFLICFAPYVMTLAEVLVFTVNAQWGILS 279
DB 247 WQ-----QRRSEKKITRLVLMVWVWVFLQWMPFVYVQLNLV-VTSLDATVNHVS 296
QY 280 KCLTYSKAVADPPFTYSL-----RPPRCVLT 305
DB 297 LILSVANSCLPILYGLFSLDNFRSRFORVL 326
RESULT 4
JN0591
serotonin receptor 6 - rat

N:Alternate names: 5-hydroxytryptamine receptor 6 (5-HTR6)

C:Species: Rattus norvegicus (Norway rat)

C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 05-Nov-1999

C:Accession: JN0591

R:Ruat, M.; Traiffort, E.; Arrang, J.M.; Tardivel-Lacombe, J.; Diaz, J.; Leurs, R.; Schwa

Biochem. Biophys. Res. Commun. 193, 268-276, 1993

A:Title: A novel rat serotonin (5-HT₆) receptor: molecular cloning, localization and st

A:Reference number: JN0591; MUID:93277562; PMID:8389146

A:Accession: JN0591

A:Molecule type: DNA

A:Residues: 1-436 <RUA>

A:Cross-references: GB:S62043; NID:G385708; PIDN:ABE26908.1; PID:G385709

C:Genetics:

A:Introns: 238/3

C:Superfamily: vertebrate rhodopsin

C:Keywords: glycoprotein; neurotransmitter receptor; transmembrane protein

F:29-53/Domain: transmembrane #status predicted <TM1>

F:63-84/Domain: transmembrane #status predicted <TM2>

F:95-122/Domain: transmembrane #status predicted <TM3>

F:141-168/Domain: transmembrane #status predicted <TM4>

F:185-213/Domain: transmembrane #status predicted <TM5>

F:267-293/Domain: transmembrane #status predicted <TM6>

F:297-319/Domain: transmembrane #status predicted <TM7>

F:9/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 12.9%; Score 239; DB 2; Length 436;

Best Local Similarity 25.7%; Pred. No. 1.9e-12;

Matches 65; Conservative 58; Mismatches 146; Indels 42; Gaps 11;

QY 2 GPGEA-----LLAGLLVNLVALLSNALVLLCCAYSAELTRASGVLLNLSLGH 53

DB 16 GPGPPAPGGSGWAAALCVIVITAAANSLIIVLICQPALNT--SNFLVSLFTSL 73

QY 54 LLAALDMPFTLLGVNRGTPAGACOVIGFDLTFASNAALSVAALSADWLAVGFPLR 113

DB 74 MVGLVMPAMNLYGRWLARGLLWTFADVMCCSASILNCLISLDLYLLISPLR 133

QY 114 YAGRL-RRYAGLLCWGOSLA----FSGALGCSWLGYSAPFASCSRLRPPERP 168

DB 134 YKLRWTPRALALIG-AW--SLAALASFLPLLGWHLGCKART-----PAPGOCR 181

QY 169 FAA---FTATLHAYGVFLPLAVLCLTSLQVHRVARRHCORMDTVT-----MKALALLA 218

DB 182 LLASLPFLVNLVAGVTFFLPSPAICFTYCRILLAAKQAVQVSLTTGTGAQLETLQVR 241

QY 219 DLHSVR-----ORCLQOKRRHRATKIGIATFLICFAPVMTLAEVLPFTVNAQ 274

DB 242 TPRGMSADSRRLATKHSRKALKASUTGLILGMFFVTWLPFFVANIAQAVDCISPL 301

QY 275 WGLSKCLITYSKAVADPFTYSLRRPFRQVL 305

DB 302 FDLVT-WLGYCNSTMNPIIYPLFMRDFKRAL 331

RESULT 5

JC4120

C:Species: Cavia porcellus (Guinea pig)

C>Date: 27-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 24-Nov-1999

C:Accession: JC4120

R:Traiffort, E.; Vizute, M.L.; Tardivel-Lacombe, J.; Souil, E.; Schwartz, J.C.; Ruat, M

Biochem. Biophys. Res. Commun. 211, 570-577, 1995

A:Title: The guinea pig histamine H2 receptor: gene cloning, tissue expression and chrom

A:Reference number: JC4120; MUID:95314628; PMID:7794271

A:Accession: JC4120

A:Molecule type: DNA

A:Residues: 1-359 <TRA>

A:Comment: Histamine, a messenger molecule in cell-to-cell communication, affects its ta

ly defined receptor subtypes named H1, H2 and H3.

C:Superfamily: vertebrate rhodopsin

C:Keywords: glycoprotein; phosphoprotein; receptor; transmembrane protein

F:22-45/Domain: transmembrane #status predicted <TM1>

F:58-81/Domain: transmembrane #status predicted <TM2>

F:93-113/Domain: transmembrane #status predicted <TM3>

F:136-157/Domain: transmembrane #status predicted <TM4>

F:179-204/Domain: transmembrane #status predicted <TM5>

F:235-236/Domain: transmembrane #status predicted <TM6>

F:269-289/Domain: transmembrane #status predicted <TM7>

F:4,162,168/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:221,316/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicte

F:226,357/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicte

Query Match 12.5%; Score 232.5; DB 2; Length 359;

Best Local Similarity 22.0%; Pred. No. 5.4e-12;

Matches 73; Conservative 67; Mismatches 139; Indels 53; Gaps 8;

QY 11 LVMVLAVALLSNALVLLCCAYSAELTRASGVLLNLSLGHLLLAALDMPFTLLGVNRG 70

DB 24 ILIILITVTVAGNVVVCVAVGLNRLRS-LTNCFIYSLAVTDLILLGLLVLPFSAIYQLSC 82

QY 71 RTPSAGCACOVIGFDLTFASNAALSVAALSADWLAVGFPLRYAGRLPRYAGLLGCA 130

DB 83 KWSFSKVPCHYIYSLDVMVLTASILNLFMSLDRYCAVTDPLRYPVLIIPARVAISLVFI 142

QY 131 WQGLAFSGAALGCSWLGY-----SSAFASCSRLRPPERPFAAFTATLHAGVFVLP 184

DB 143 WVISITLSFLSIHLGMNSRNETSKNDITVCKVQVN-----EYVGLVDGLVTFYLP 194

QY 185 LAVLCLTSLQVHRVARRHCORMDTV-TMKALALLADLHPVSRQCLIQOKRRHRATRKI 243

DB 195 LLIMCIYIFRIFKAREQARRINHGSKRAATI-----REHKATVTL 236

QY 244 GIAIATFLICFAPVMTLAEVLPFV-----TNAWGILSKCLITYSKAVADPFTYS 295

DB 237 AAVNGARFIICFFPY-----FTVFYRGLKGDVAINEVFEDVVLWGLVANSALNPILYA 289

QY 296 LLRRPFRQVLAVMVRLLKRTPRFASHTDSSL 327

DB 290 ALNEDFRTA----YHQLFCCRLASHNSHETSLS 317

RESULT 6

JN0763

C:Species: Homo sapiens (man)

C>Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 20-Jun-2000

C:Accession: JN0763

R:Yamada, Y.; Kagimoto, S.; Kubota, A.; Yasuda, K.; Masuda, K.; Someya, Y.; Ihara, Y.; Li

Biochem. Biophys. Res. Commun. 195, 844-852, 1993

A:Title: Cloning, functional expression and pharmacological characterization of a fourth

A:Reference number: JN0762; MUID:93384611; PMID:8373420

A:Accession: JN0763

A:Molecule type: DNA

A:Residues: 1-364 <YAM>

A:Cross-references: DDBJ:D16827; NID:G487683; PIDN:BA04107.1; PID:G487684

A:Comment: This protein is a member of somatostatin receptor family.

C:Genetics:

A:Gene: GDB:SSTR5

A:Cross-references: GDB:138452; OMIM:182455

A:Map position: 16p13.3-16p13.3

A:Introns: #status absent

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; glycoprotein; lipoprotein; phosphoprotein; thiole

F:40-66/Domain: transmembrane #status predicted <TM1>

F:77-102/Domain: transmembrane #status predicted <TM2>

F:114-135/Domain: transmembrane #status predicted <TM3>

F:155-177/Domain: transmembrane #status predicted <TM4>

F:196-228/Domain: transmembrane #status predicted <TM5>

F:246-273/Domain: transmembrane #status predicted <TM6>

F:280-307/Domain: transmembrane #status predicted <TM7>

F:13, 26, 187/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:112-186/Disulfide bonds: #status predicted

F:242,325/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status pr

F:247/Binding site: phosphate (Thr) (covalent) (by cAMP-dependent kinase) #status predict

F:320/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match 12.5%; Score 231.5; DB 2; Length 364;
 Best Local Similarity 25.0%; Pred. No. 6.6e-12;
 Matches 92; Conservative 51; Mismatches 166; Indels 59; Gaps 11;

QY 2 GPGEALLAGLVVAVLAVALLSNALVLLCCAYSAELRTRASGVLLVNLISLGHLLAALDMP 61
 DB 37 GARAVLPVLYLVCAAGLGNTLVIVVLRFAKMT-VTNIYINLAVADVLY-MLGLP 94
 QY 62 FTLLGVNRGRTSPAGACQVIGFDTFLASNAALSVAALSADQWLAVGFFLYAGRLRPR 121
 DB 95 FLATQNAASFPPFGPVLCLVMTLDGNOFTSVFCLTVMSVDVRYLAVVHPPLSSARWRPR 154
 QY 122 YAGLLGCAMGQSLAFS-----GAALGCSMLGYSSAFASCSRLRPPERPFA 170
 DB 155 VAKLASAAAVLSLCHMSLPLLVADYVQEGTGNASW-----PEPVGLWGA 199
 QY 171 APTATLHAGVFLVPLAVLCUTLSQVHRVARRHCQMDVTMKALALLADLHPSVQRCL 230
 DB 200 VFIYITAVLGFFAPLVLICL-----CYLLIVVKVRA-----AGVRVGCV- 238
 QY 231 QOKRRRHRAFKIGIAIATFLICFAPYV---MTRLAELVPFVTVAQWGLSKCLITYSKA 287
 DB 239 -RRSERKVTMVLVVLVPAGCWLFFFTVINVNLAVLPQEPASAGLYFFVWILSYANS 297
 QY 288 VADPFTYSLRRPFRQVLAGMVRHLKTRPRPASTHSDSLDVAGMWHQLLKRT-PRPAST 346
 DB 298 CANPVLGYGLSDNFRSQFKV---LCLRKSGAKADATEPRPDRIROOQATPRTA 353
 QY 346 THNGSVDT 353
 DB 354 ANGLMOT 361

RESULT 7
 157955
 somatostatin receptor - human
 C:Species: Homo sapiens (man)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Nov-1999
 X:Panetta, R.; Greenwood, M.T.; Warszynska, A.; Demchysyn, L.L.; Day, R.; Niznik, H.B.;
 Mol. Pharmacol. 45, 417-427, 1994
 A:Title: Molecular cloning, functional characterization, and chromosomal localization of
 A:Reference number: 157955; MUID:94195267; PMID:7908405
 A:Accession: 157955
 A:Status: preliminary; translated from GB/EMBL/DDDBJ
 A:Molecule type: DNA
 A:Residues: 1-363 <RES>
 A:Cross-references: GB:L14865; NID:9431094; PIDN:AAA0828.1; PID:g431095
 C:Genetics:
 A:Gene: GDB:SST
 A:Cross-references: GDB:119604; OMIM:182450
 A:Map position: 3q28-3q28
 C:Superfamily: vertebrate rhodopsin

Query Match 12.4%; Score 231; DB 2; Length 363;
 Best Local Similarity 25.1%; Pred. No. 7.2e-12;
 Matches 92; Conservative 51; Mismatches 166; Indels 58; Gaps 11;

QY 2 GPGEALLAGLVVAVLAVALLSNALVLLCCAYSAELRTRASGVLLVNLISLGHLLAALDMP 61
 DB 37 GARAVLPVLYLVCAAGLGNTLVIVVLRFAKMT-VTNIYINLAVADVLY-MLGLP 94
 QY 62 FTLLGVNRGRTSPAGACQVIGFDTFLASNAALSVAALSADQWLAVGFFLYAGRLRPR 121
 DB 95 FLATQNAASFPPFGPVLCLVMTLDGNOFTSVFCLTVMSVDVRYLAVVHPPLSSARWRPR 154
 QY 122 YAGLLGCAMGQSLAFS-----GAALGCSMLGYSSAFASCSRLRPPERPFA 170
 DB 155 VAKLASAAAVLSLCHMSLPLLVADYVQEGTGNASW-----PEPVGLWGA 199
 QY 171 APTATLHAGVFLVPLAVLCUTLSQVHRVARRHCQMDVTMKALALLADLHPSVQRCL 230
 DB 200 VFIYITAVLGFFAPLVLICL-----CYLLIVVKVRA-----AGVRVGCV- 238

QY 231 QOKRRRHRAFKIGIAIATFLICFAPYV---MTRLAELVPFVTVAQWGLSKCLITYSKA 287
 DB 239 -RRSERKVTMVLVVLVVFACGWLFFFTVINVNLAVLPQEPASAGLYFFVWILSYANS 297
 QY 288 VADPFTYSLRRPFRQVLAGMVRHLKTRPRPASTHSDSLDVAGMWHQLLKRT-PRPAST 346
 DB 298 CANPVLGYGLSDNFRSQFKV---LCLRKSGAKADATEPRPDRIROOQATPRTA 354
 QY 347 HNGSVDT 353
 DB 355 -NGLMOT 360

RESULT 8
 QHUBE
 beta-3-adrenergic receptor, splice form 3 - human
 N:Alternate names: beta-3-adrenergic receptor form B
 N:Contents: beta-3-adrenergic receptor splice form 1
 C:Species: Homo sapiens (man)
 C:Date: 03-Feb-1994 #sequence_revision 18-Aug-1995 #text_change 16-Jun-2000
 C:Accession: S33751; S33753; S32803; S32826
 R:Leiss, J.M.; Kaghad, M.; Rodriguez, M.; Chalon, P.; Bonnin, J.; Dupre, I.; Delpech, B.
 FEBS Lett. 324, 127-130, 1993
 A:Title: Molecular cloning of a human beta-3-adrenergic receptor cDNA.
 A:Reference number: S33751; MUID:93285320; PMID:8389717
 A:Accession: S33751
 A:Molecule type: mRNA
 A:Residues: 1-408 <LEL1>
 A:Cross-references: EMBL:X70811; NID:g312396; PIDN:CAA50141.1; PID:g312397
 A:Note: Splice form 3
 A:Molecule type: DNA
 A:Residues: 392-408 <LEL2>
 A:Cross-references: GB:X70812; NID:g312398; PIDN:CAA50143.1; PID:g1666376
 R:Emorine, L.J.
 submitted to the EMBL Data Library, March 1993
 A:Reference number: S32803
 A:Molecule type: DNA
 A:Residues: 1-408 <EMO>
 A:Cross-references: EMBL:X72861; NID:g98094; PIDN:CAA51383.1; PID:g298095
 R:van Spronsen, A.; Nahmias, C.; Krief, S.; Briand-Sutren, M.M.; Strosberg, A.D.; Emorine
 Eur. J. Biochem. 213, 1117-1124, 1993
 A:Title: The promoter and intron/exon structure of the human and mouse beta3-adrenergic-1
 A:Reference number: S32826; MUID:93279311; PMID:8389293
 A:Accession: S32826
 A:Molecule type: DNA
 A:Residues: 1-87344-350;394-408 <SPR>
 C:Genetics:
 A:Gene: GDB:ADRB3
 A:Cross-references: GDB:203869; OMIM:109691
 A:Map position: 8p12-8p11.1
 A:Introns: 402/2
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane
 F:1-408/Product: beta-3-adrenergic receptor precursor splice form 3 #status predicted <W>
 F:1-402/Product: beta-3-adrenergic receptor precursor splice form 1 #status predicted <W>
 F:37-63/Domain: transmembrane #status predicted <TM1>
 F:73-101/Domain: transmembrane #status predicted <TM2>
 F:113-133/Domain: transmembrane #status predicted <TM3>
 F:156-178/Domain: transmembrane #status predicted <TM4>
 F:204-225/Domain: transmembrane #status predicted <TM5>
 F:293-314/Domain: transmembrane #status predicted <TM6>
 F:327-347/Domain: transmembrane #status predicted <TM7>
 F:8,26/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 12.4%; Score 230.5; DB 1; Length 408;
 Best Local Similarity 24.9%; Pred. No. 9e-12;
 Matches 93; Conservative 61; Mismatches 154; Indels 65; Gaps 14;

QY 3 PGEALLAGLVVAVLAVALLSNALVLLCCAYSAELRTRASGVLLVNLISLGHLLAAL 58

Db 34 PWEAALAGAL---LALAVLATVGGNLLVIVAIAWTPRLQT-MTNVFTVSLAAADLVWGLL 89
QY 59 DMPFTLLGVMRGRTSPAGCAQVIGFLDTFLASNAALSAALSDQWLAVGFPRLRYAGRL 118
Db 90 VVPPAATLALTGHWPGLGATGCELTWSDVLCVETLCAVADRYLAVTNPLRYGALV 149
QY 119 RPRVAGLLGCAGQSLAFSGAALGCSW--LGYSASFASCSLRPLPPEPRPFAAFTATL 176
Db 150 TKRCARTAVLVWVVAASVAFIPMSQWRVGADEAQRCH-----SNPRCCAFASNM 202
QY 177 -----HAGVFVLPLAVLCLTSLQVHRVARRHC-----QRMDTVTKALA--- 215
Db 203 PYVLLSSVSFYLLPLVLMFVYARVFWATRLRLRGELGRFPPEPPAPSRSLAPAP 262
QY 216 ----LLADLHPSVRORCLTQKRRHRATRKIGIAIATFLICFAPYVMTL-----AEL 265
Db 263 VGTCAPEGVPACGRPARLLPLREHRLCTGLIMGTFTLCWLPFLANVLRAALGGPSL 322
QY 266 VP---FVTVNAQWGLSKCLTYSKAVADPFTYSL---LRRPQVLAGVHRLKTRPR 319
Db 323 VPGPAFLALN-W-----LGYSANAFNPLIYCRSPDPSAFRLLRCGRRL---PPEP 371
QY 320 ASTHDSLLDVAGM 332
Db 372 CAARPALFPFSGV 384
RESULT 9
ORHUB3
beta-3-adrenergic receptor, splice form 2 - human
N;Alternate names: beta-3-adrenergic receptor form A
N;Contains: beta-3-adrenergic receptor splice form 1
C;Species: Homo sapiens (man)
C;Date: 22-Jan-1993 #sequence_revision 18-Aug-1995 #text_change 16-Jun-2000
R;Accession: A41348; S33752
R;Emorine, L.J.; Marullo, S.; Briand-Sutren, M.M.; Patey, G.; Tate, K.; Delavier-Klutch
Science 245, 1118-1121, 1989
A;Title: Molecular characterization of the human beta-3-adrenergic receptor.
A;Reference number: A41348; PMID:89368947; PMID:2570461
A;Status: nucleic acid sequence not shown
A;Accession: A41348
A;Molecule type: DNA
A;Residues: 1-402 <BMO>
A;Cross-references: GB:M29932; NID:G178895; PIDN:AAA35550.1; PID:G178896
A;Note: splice form 1
R;Leillas, J.M.; Kagnad, M.; Rodriguez, M.; Chalon, P.; Bonnin, J.; Dupre, I.; Delpech, E
FEBS Lett. 324, 127-130, 1993
A;Title: Molecular cloning of a human beta-3-adrenergic receptor cDNA.
A;Reference number: S33751; PMID:93285320; PMID:8389717
A;Accession: S33752
A;Molecule type: DNA
A;Residues: 32-414 <LEL>
A;Cross-references: EMBL:X70812; NID:G312398; PIDN:CAA50142.1; PID:G1666375
A;Note: splice form 2
C;Genetics:
A;Gene: GDB:ADRB3
A;Cross-references: GDB:203869; OMIM:109691
A;Map position: 8p12-8p11.1
A;Introns: 402/2
C;Superfamily: vertebrate rhodopsin
C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembran
F;1-414/Product: beta-3-adrenergic receptor precursor splice form 2 #status predicted <M
F;1-402/Product: beta-3-adrenergic receptor precursor splice form 1 #status predicted <M
F;37-63/Domain: transmembrane #status predicted <TM1>
F;73-101/Domain: transmembrane #status predicted <TM2>
F;113-133/Domain: transmembrane #status predicted <TM3>
F;156-178/Domain: transmembrane #status predicted <TM4>
F;204-225/Domain: transmembrane #status predicted <TM5>
F;293-314/Domain: transmembrane #status predicted <TM6>
F;327-347/Domain: transmembrane #status predicted <TM7>
F;8,26/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

12.4%; Score 230.5; DB 1; Length 414;

Best Local Similarity 24.9%; Pred. No. 9.2e-12;
Matches 93; Conservative 61; Mismatches 154; Indels 65; Gaps 14;
QY 3 PGEALLAGLLVWVLAVALLS-----NALVLLCCAYSALRTRASGVLLVNLISLGHLLAAL 58
Db 34 PWEAALAGAL---LALAVLATVGGNLLVIVAIAWTPRLQT-MTNVFTVSLAAADLVWGLL 89
QY 59 DMPFTLLGVMRGRTSPAGCAQVIGFLDTFLASNAALSAALSDQWLAVGFPRLRYAGRL 118
Db 90 VVPPAATLALTGHWPGLGATGCELTWSDVLCVETLCAVADRYLAVTNPLRYGALV 149
QY 119 RPRVAGLLGCAGQSLAFSGAALGCSW--LGYSASFASCSLRPLPPEPRPFAAFTATL 176
Db 150 TKRCARTAVLVWVVAASVAFIPMSQWRVGADEAQRCH-----SNPRCCAFASNM 202
QY 177 -----HAGVFVLPLAVLCLTSLQVHRVARRHC-----QRMDTVTKALA--- 215
Db 203 PYVLLSSVSFYLLPLVLMFVYARVFWATRLRLRGELGRFPPEPPAPSRSLAPAP 262
QY 216 ----LLADLHPSVRORCLTQKRRHRATRKIGIAIATFLICFAPYVMTL-----AEL 265
Db 263 VGTCAPEGVPACGRPARLLPLREHRLCTGLIMGTFTLCWLPFLANVLRAALGGPSL 322
QY 266 VP---FVTVNAQWGLSKCLTYSKAVADPFTYSL---LRRPQVLAGVHRLKTRPR 319
Db 323 VPGPAFLALN-W-----LGYSANAFNPLIYCRSPDPSAFRLLRCGRRL---PPEP 371
QY 320 ASTHDSLLDVAGM 332
Db 372 CAARPALFPFSGV 384
RESULT 10
G02953
beta-3-adrenergic receptor - rhesus macaque
C;Species: Macaca mulatta (rhesus macaque)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 13-Aug-1999
C;Accession: G02953
R;Lowe, A.L.; Walston, J.; Shuldiner, A.R.
submitted to the EMBL Data Library, July 1996
A;Reference number: H01989
A;Accession: G02953
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-418 <LOW>
A;Cross-references: EMBL:U63592; NID:G1458230; PIDN:AAB53939.1; PID:G1458232
C;Genetics:
A;Introns: 402/1
C;Superfamily: vertebrate rhodopsin
Query Match 12.4%; Score 229.5; DB 2; Length 418;
Best Local Similarity 25.9%; Pred. No. 1.1e-11;
Matches 95; Conservative 56; Mismatches 149; Indels 67; Gaps 15;
QY 3 PGEALLAGLLVWVLAVALLS-----NALVLLCCAYSALRTRASGVLLVNLISLGHLLAAL 58
Db 34 PWEAALAGAL---LALAVLATVGGNLLVIVAIAWTPRLQT-MTNVFTVSLAAADLVWGLL 89
QY 59 DMPFTLLGVMRGRTSPAGCAQVIGFLDTFLASNAALSAALSDQWLAVGFPRLRYAGRL 118
Db 90 VVPPAATLALTGHWPGLGATGCELTWSDVLCVETLCAVADRYLAVTNPLRYGALV 149
QY 119 RPRVAGLLGCAGQSLAFSGAALGCSW--LGYSASFASCSLRPLPPEPRPFAAFTATL 176
Db 150 TKRCARTAVLVWVVAASVAFIPMSQWRVGADEAQRCH-----SNPRCCAFASNM 202
QY 177 -----HAGVFVLPLAVLCLTSLQVHRVARRHC-----QRMDTVTKALA--- 224
Db 203 PYVLLSSVSFYLLPLVLMFVYARVFWATRLRLRGELGRFPPEPPAPSRSLAPAP 262
QY 225 RQRCLIQ-----KRRHRATRKIGIAIATFLICFAPYVMTL-----AEL 265
Db 263 AGTCAPPEGVACCRPARLLPLREHRLCTGLIMGTFTLCWLPFLANVLRAALGGPSL 322

C41795
somatostatin receptor 1 - mouse
C/Species: Mus musculus (house mouse)
C/Date: 30-Sep-1993 #sequence_revision 31-Dec-1993 #text_change 24-Nov-1999
C/Accession: C41795
R/Yamada, Y.; Post, S.R.; Wang, K.; Tager, H.S.; Bell, G.I.; Seino, S.
Proc. Natl. Acad. Sci. U.S.A. 89, 251-255, 1992
A/Title: Cloning and functional characterization of a family of human and mouse somatostatin receptors
A/Reference number: A41795; MUID:92108031; PMID:11346068
A/Accession: C41795
A/Status: nucleic acid sequence not shown
A/Molecule type: DNA
A/Residues: 1-391 <VAM>
A/Cross-references: GB:M81831; NID:g201058; PIDN:AAA58255.1; PID:g201059
A/Keywords: G protein-coupled receptor; hormone receptor; transmembrane protein

Query Match 12.3%; Score 228.5; DB 2; Length 391;
Best Local Similarity 24.5%; Pred. No. 1.3e-11;
Matches 78; Conservative 61; Mismatches 131; Indels 49; Gaps 11;

QY 2 GPEALLAGLLVMVLA-VALLSNALVLLCCAYSAELRTRASGVLLVNLISLGHLLAALDM 60
DB 54 GQSAILISFIYSVCLVGLCGNSMWIYILRYAKMT-ATNIYILNLAIDELL-MLSV 111
QY 61 PFTLLGVNRGRTSPAGCACQVIGFLDTFLASNAALSVAALSADQWLAVGFFPLRYAGRLRP 120
DB 112 PFLVSTLLRHWPFGALLCRVLSDVAVNMFTSIYCLTVLSVDVRYAVVHPIKAARYRP 171
QY 121 RYAGLLGCWAGQSL-----AFSGAALGCSWLGSSAFASCSRLRPPPERPFAAPT 173
DB 172 TVAKVNLGVNVLSSLLVILPIVVFSTRAN-----SDGTVACNM-LMPEPAQRLWLVGFV 224
QY 174 ATLHVGFLPLAVLCITSLQVHRVARRHCQMDVTMKALLADLHPSVRQCLIQOK 233
DB 225 LYTFMGFLPLVGAICL-----CYVLIANKRWVAKAGWQ-----QRK 263
QY 234 RRRHRTKIGIAIATFLICFAPVYMTRELAVL---PFVTVNAQWGLSKCLITYSKAVD 290
DB 264 RSEKRTILMVMVMVVFICWMPFYVQLVNFAEQDQATVSQ----LSVILGYANSCAN 319
QY 291 PFTYSLL---RRPFRQVL 305
DB 320 PLYGFLSDNFKRSFORIL 338

RESULT 14
A39297
somatostatin receptor - rat
N/Alternate names: probable G-protein-coupled receptor; SRIF receptor
C/Species: Rattus norvegicus (Norway rat)
C/Date: 03-Aug-1992 #sequence_revision 03-Aug-1992 #text_change 24-Nov-1999
C/Accession: A39297; A45102; S20088
R/Meyerhof, W.; Paust, H.J.; Schoenrock, C.; Richter, D.
DNA Cell Biol. 10, 689-694, 1991
A/Title: Cloning of a cDNA encoding a novel putative G-protein-coupled receptor expressed in rat brain
A/Reference number: A39297; MUID:92096119; PMID:1861599
A/Accession: A39297
A/Molecule type: mRNA
A/Residues: 1-391 <MEY>
A/Cross-references: GB:X62314; GB:X61630; NID:g56309; PIDN:CAA44193.1; PID:g56310
A/Experimental source: brain
A/Note: it is uncertain whether Met-1 is the initiator or whether translation is initiated at Met-2
R/Li, X.J.; Forte, M.; North, R.A.; Ross, C.A.; Snyder, S.H.
J. Biol. Chem. 267, 21307-21312, 1992
A/Title: Cloning and expression of a rat somatostatin receptor enriched in brain.
A/Reference number: A45102; MUID:93016064; PMID:1400442
A/Accession: A45102
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: nucleic acid
A/Residues: 1-391 <LII>
A/Experimental source: brain
A/Note: sequence extracted from NCBI backbone (NCBIP:116692)

C/Superfamily: vertebrate rhodopsin
C/Keywords: G protein-coupled receptor; glycoprotein; receptor; transmembrane protein

Query Match 12.3%; Score 228.5; DB 2; Length 391;
Best Local Similarity 24.5%; Pred. No. 1.3e-11;
Matches 78; Conservative 61; Mismatches 131; Indels 49; Gaps 11;

QY 2 GPEALLAGLLVMVLA-VALLSNALVLLCCAYSAELRTRASGVLLVNLISLGHLLAALDM 60
DB 54 GQSAILISFIYSVCLVGLCGNSMWIYILRYAKMT-ATNIYILNLAIDELL-MLSV 111
QY 61 PFTLLGVNRGRTSPAGCACQVIGFLDTFLASNAALSVAALSADQWLAVGFFPLRYAGRLRP 120
DB 112 PFLVSTLLRHWPFGALLCRVLSDVAVNMFTSIYCLTVLSVDVRYAVVHPIKAARYRP 171
QY 121 RYAGLLGCWAGQSL-----AFSGAALGCSWLGSSAFASCSRLRPPPERPFAAPT 173
DB 172 TVAKVNLGVNVLSSLLVILPIVVFSTRAN-----SDGTVACNM-LMPEPAQRLWLVGFV 224
QY 174 ATLHVGFLPLAVLCITSLQVHRVARRHCQMDVTMKALLADLHPSVRQCLIQOK 233
DB 225 LYTFMGFLPLVGAICL-----CYVLIANKRWVAKAGWQ-----QRK 263
QY 234 RRRHRTKIGIAIATFLICFAPVYMTRELAVL---PFVTVNAQWGLSKCLITYSKAVD 290
DB 264 RSEKRTILMVMVMVVFICWMPFYVQLVNFAEQDQATVSQ----LSVILGYANSCAN 319
QY 291 PFTYSLL---RRPFRQVL 305
DB 320 PLYGFLSDNFKRSFORIL 338

RESULT 15
DYNHDS
dopamine receptor D5 - human
C/Species: Homo sapiens (man)
C/Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 22-Jun-1999
C/Accession: S15080; A41232
R/Sunahara, R.K.; Guan, H.C.; O'Dowd, B.F.; Seeman, P.; Laurie, L.G.; Ng, G.; George, S.
Nature 350, 614-619, 1991
A/Title: Cloning of the gene for a human dopamine D(5) receptor with higher affinity for dopamine
A/Reference number: S15080; MUID:91204055; PMID:1826762
A/Accession: S15080
A/Molecule type: DNA
A/Residues: 1-477 <SUN>
A/Cross-references: EMBL:X58454; NID:g32048; PIDN:CAA1360.1; PID:g32049
R/Grandy, D.K.; Zhang, Y.; Bouvier, C.; Zhou, Q.Y.; Johnson, R.A.; Allen, L.; Buck, K.; I
Proc. Natl. Acad. Sci. U.S.A. 88, 9175-9179, 1991
A/Title: Multiple human D-5 dopamine receptor genes: a functional receptor and two pseudogenes
A/Reference number: A41232; MUID:92021013; PMID:1833775
A/Accession: A41232
A/Molecule type: DNA
A/Residues: 1-477 <GRA>
A/Cross-references: GB:M67439; NID:g181830; PIDN:AAA52329.1; PID:g181831
C/Genetics:
A/Gene: GDB:DRD5; DRD12
A/Cross-references: GDB:127548; OMIM:126453
A/Map position: 4p15.3-4p15.1
C/Superfamily: vertebrate rhodopsin
C/Keywords: G protein-coupled receptor; glycoprotein; lipoprotein; neurotransmitter receptor
F.78-104/Domain: transmembrane #status predicted <TM1>
F.115-136/Domain: transmembrane #status predicted <TM3>
F.157-180/Domain: transmembrane #status predicted <TM4>
F.225-245/Domain: transmembrane #status predicted <TM5>
F.246-297/Domain: intracellular #status predicted <INT>
F.298-319/Domain: transmembrane #status predicted <TM6>
F.341-361/Domain: transmembrane #status predicted <TM7>
F.7.199/Binding site: carbohydrate (Aen) (covalent) #status predicted
F.113-217/Disulfide bonds: #status predicted
F.153,252/Binding site: phosphate (Thr) (covalent) #status predicted
F.260,271,283/Binding site: phosphate (Ser) (covalent) #status predicted
F.375/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match 12.3%; Score 228.5; DB 1; Length 477;
Best Local Similarity 21.6%; Pred. No. 1.6e-11;
Matches 90; Conservative 82; Mismatches 162; Indels 83; Gaps 17;

Qy	1	MPGEGALLAGLLVMVLAVALLSNALVLLCCAYSAELRTRASGVLLVNLGLHLLAALDM	60
Db	36	LGPSQVVTACLLTLIIITLLGNVLCVCAAIIVRSRHLRANMTNFIIVSLAVSDLFVALLVM	95
Qy	61	PFTLLGVNRGRTPSAGA-COVIGFLDTFLASNAALSVAALSADQWLAVGFFPLRYAGRRLR	119
Db	96	PKKAVAEVAGYWP--GAFCDVWVAFDIMCSTASILNLCVISVDRYWAIISRPFRYKRW	153
Qy	120	PRYAGLLGCGWGLAFSGAALGCSWLGYSAPASCSLRLLP-----EPE-165	
Db	154	QRMALVMVGLAWTLISILISFTIPVQLNW-HRDQAASWGGLDLPNNLANWTPEEDFWEPDV	212
Qy	166	-----RPFPAFTATLHAGVFLPLAVLCLTSLOVHRVARRHCORMDVTMKA----	213
Db	213	NAENCDSINRTYAISSL--ISFYIPVAINIVTYIRIYIAQVQIRRISSLERAEHAQ	270
Qy	214	-LALLADLHPSVRQRCILQQRHRRATRKIGIAIATFLICFAPYVMTRLAELVPFVTVN	272
Db	271	SCRSSAACAPDTSLRASI---KQTKVLKTLSTVMGVGCWLPFFI--LNCMVPPFCSGH	325
Qy	273	AQ-----WGILSKCLTYSKAVADPFTYSL---LRPFRQVLAGMVHR	311
Db	326	PEGPPAGFPVCVSETTFVFW-----FGWANSINPVIYAFNADFOKFAQLL-GCSH-	377
Qy	312	LLKETPRPASTHDSLSL-----DV-----AGMVHQLLKETPRPASTHNGSVDTEND	356
Db	378	FCSRTPTVETVNISNELISYNQDIVFKHEIAAAAYTHW----PNAVTPGNREVDNDEE	430

Search completed: May 18, 2004, 12:08:40
Job time : 21 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 18, 2004, 12:01:36 ; Search time 18 Seconds
(without alignments)
1050.081 Million cell updates/sec

Title: US-10-049-569-2
Perfect score: 1858
Sequence: 1 MGFALLAGLLVWVLAVAL.....ASTNGSVDTENDSLQOOTH 363

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1843	99.2	363	GP78 HUMAN	Q96P69 homo sapien
2	848	45.6	337	GP26 HUMAN	Q8ndv2 homo sapien
3	823	44.3	337	GP26 RAT	Q9bx13 rattus norv
4	822	44.2	337	GP26 MOUSE	Q8bza7 mus musculu
5	245.5	13.2	440	SH6 MOUSE	Q9rlc8 mus musculu
6	244.5	13.2	440	SH6 HUMAN	P50406 homo sapien
7	243.5	13.1	388	SH6 HUMAN	P31391 homo sapien
8	239.9	12.9	436	SH6 RAT	P31388 rattus norv
9	232.5	12.5	359	HH2R CAVPO	P47747 cavia porce
10	232	12.5	388	SH4 MOUSE	P97288 mus musculu
11	231.5	12.5	364	SSR5 HUMAN	P35346 homo sapien
12	230.5	12.4	408	B3AR HUMAN	P13945 homo sapien
13	229.5	12.4	418	B3AR MACMU	Q28524 macaca mula
14	229.5	12.4	425	OX1R HUMAN	Q43613 homo sapien
15	229.9	12.3	362	SSR5 MOUSE	O08858 mus musculu
16	228.5	12.3	363	SSR5 RAT	P30938 rattus norv
17	228.5	12.3	391	SSR1 HUMAN	P30872 homo sapien
18	228.5	12.3	391	SSR1 MOUSE	P30872 mus musculu
19	228.5	12.3	391	SSR1 RAT	P28646 rattus norv
20	228.5	12.3	477	DBDR HUMAN	P21918 homo sapien
21	228	12.3	387	DBDR HUMAN	Q43603 homo sapien
22	228	12.3	475	DBDR RAT	P25115 rattus norv
23	224.5	12.1	358	HH2R MOUSE	P97292 mus musculu
24	224	12.1	372	GALS RAT	O08726 rattus norv
25	224	12.1	457	DBDR XENLA	P42290 xenopus lae
26	224	12.1	514	AIAB MOUSE	P97717 mus musculu
27	223.5	12.0	359	HH2R CANFA	P17124 canis famil
28	223	12.0	369	SSR2 HUMAN	P30874 homo sapien
29	223	12.0	388	SH4 CAVPO	O70528 cavia porce
30	223	12.0	467	BIAR BOVIN	Q9ct96 bos taurus
31	223	12.0	479	SH7 HUMAN	P34969 homo sapien
32	222.5	12.0	384	SSR4 RAT	P30937 rattus norv
33	222.5	12.0	561	AIAD RAT	P23944 rattus norv

ALIGNMENTS

RESULT 1									
GP78 HUMAN									
ID	GP78 HUMAN	STANDARD;		PRT;	363 AA.				
AC	Q96P69; Q8NGV3;								
DT	10-OCT-2003 (Rel. 42, Created)								
DT	10-OCT-2003 (Rel. 42, Last sequence update)								
DT	10-OCT-2003 (Rel. 42, Last annotation update)								
DE	Probable G protein-coupled receptor GPR78.								
GN	GPR78.								
OS	Homo sapiens (Human).								
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.								
OX	NCBI_TaxID=9606;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RX	MEDLINE=21458557; PubMed=11574155;								
RA	Lee D.K., Nguyen T., Lynch K.R., Cheng R., Vanti W.B., Arkhitko O.,								
RA	Lewis T., Evans J.E., George S.R., O'Dowd B.F.;								
RT	"Discovery and mapping of ten novel G protein-coupled receptor								
RT	genes";								
RL	Gene 275:83-91(2001).								
RN	[2]								
RP	SEQUENCE FROM N.A.								
RA	Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,								
RA	Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;								
RT	"Genome-wide discovery and analysis of human seven transmembrane helix								
RT	receptor genes";								
RL	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.								
RN	[3]								
RP	INDUCTION								
RX	MEDLINE=20175424; PubMed=10708769;								
RA	van Laar T., Schouten T., Hoogervorst E., van Eck M., van der Eb A.J.,								
RA	Terleth C.;								
RT	"The novel WMS-inducible gene Mif1/KIAA0025 is a target of the								
RT	unfolded protein response pathway.";								
RL	FEBS Lett. 469:123-131(2000).								
CC	-1- FUNCTION: Orphan receptor.								
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.								
CC	-1- TISSUE SPECIFICITY: Expressed in pituitary and placenta. No								
CC	expression detected in brain, skeletal muscle, lung, heart, liver,								
CC	pancreas, or kidney.								
CC	-1- INDUCTION: Expression increased in fibroblasts or HeLa cells								
CC	following UV-A irradiation, exposure to DNA-alkylating agents, or								
CC	endoplasmic reticulum (ER) stress caused by osmotic shock or the								
CC	glycosylation inhibitor tunicamycin.								
CC	-1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.								
CC	-----								
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CC	use by non-profit institutions as long as its content is in no way								
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/								
CC	or send an email to license@isb-sib.ch).								
CC	-----								
DR	EMBL; AF411107; AAL26479.1; -.								

P30680 rattus norv
Q13639 homo sapien
P32305 rattus norv
P53452 fugu rubrip
O88854 mus musculu
P34994 sus scrofa
P25021 homo sapien
P50021 pan troglod
P31387 mus musculu
Q91175 oryzias lat
P97714 mus musculu
O02662 canis famil

DR EMBL; AB065673; BAC05898.1; --
 DR Genew; HGNC:4528; GPR78.
 DR MIM; 606921; --
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm 1; 1.
 DR PRINTS; PRO0237; GPCRHOOPS.
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR F1.1; FALSE_NEG.
 DR PROSITE; PS00262; G-PROTEIN RECEPTOR F1.2; 1.
 KW G-protein coupled receptor; Transmembrane.
 FT DOMAIN 1 7
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 8 28
 FT DOMAIN 29 47
 FT CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 48 68
 FT DOMAIN 69 80
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 81 101
 FT DOMAIN 102 122
 FT CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 123 143
 FT DOMAIN 144 163
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 169 199
 FT DOMAIN 200 242
 FT CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 243 263
 FT DOMAIN 264 277
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 278 297
 FT DOMAIN 298 363
 FT DISULFID 79 156
 FT CONFLICT 216 216
 FT CONFLICT 226 227
 V -> L (IN REF. 2).
 HG -> OR (IN REF. 2).
 SQ SEQUENCE 363 AA; 39228 MW; 00B6D9F7E768E0ED CRC64;

Query Match 99.2%; Score 1843; DB 1; Length 363;
 Best Local Similarity 99.2%; Pred. No. 4.4e-130;
 Matches 360; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGPGALLAGLLVMVLAVALLSNALVLLCCAYSSELTRASGVLLVNLGLHLLAALDM 60
 DB 1 MGPGALLAGLLVMVLAVALLSNALVLLCCAYSSELTRASGVLLVNLGLHLLAALDM 60
 QY 61 PFTLLGVNRGRTSPAPGACQVIGFLDTFLASNAALSVAALSADQWLAVGPFPLRYAGRLRP 120
 DB 61 PFTLLGVNRGRTSPAPGACQVIGFLDTFLASNAALSVAALSADQWLAVGPFPLRYAGRLRP 120
 QY 121 RYAGLLGCAGQSLAFSGAALGCSWLGYSAPFASCSLRLPPEPRPFAATLHVG 180
 DB 121 RYAGLLGCAGQSLAFSGAALGCSWLGYSAPFASCSLRLPPEPRPFAATLHVG 180
 QY 181 FVLPLAVLCLSLQVHRVARHCQRMDDVTVMKALAVLADLHPSVRCGLIQKKRRHRAT 240
 DB 181 FVLPLAVLCLSLQVHRVARHCQRMDDVTVMKALAVLADLHPSVRCGLIQKKRRHRAT 240
 QY 241 RKIGIAITFLICFAPYVMTLAEVLVPTVNAQNGILSKCLTYSKAVADPFTVSLRRP 300
 DB 241 RKIGIAITFLICFAPYVMTLAEVLVPTVNAQNGILSKCLTYSKAVADPFTVSLRRP 300
 QY 301 FRQVLAVHRLKRTTPRSTHSSLDVAGVHQLKRTTPRSTHNGSVDTENDSCLO 360
 DB 301 FRQVLAVHRLKRTTPRSTHSSLDVAGVHQLKRTTPRSTHNGSVDTENDSCLO 360
 QY 361 QTH 363
 DB 361 QTH 363

RESULT 2

GP26 HUMAN
 ID GP26 HUMAN STANDARD; PRT; 337 AA.
 AC Q8NDV2.
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Probable G protein-coupled receptor GPR26.
 GN GPR26.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Jones G., Boulay J.L., Maier D., Merlo A.;
 RT "Sequence of the human homologue of the rat orphan G protein-coupled
 receptor GPR26 mRNA";
 RL Submitted (AUG-2002) to the EMBL/GenBank/DBSJ databases.
 [2]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Brain;
 RC Boulay J.L., Labuhn M., Jones G., Maier D., Merlo A.;
 RA "The 10q25.3-26.1 gene encoding the orphan G protein-coupled receptor
 GPR26 is epigenetically silenced in human gliomas";
 RT Submitted (AUG-2002) to the EMBL/GenBank/DBSJ databases.
 RL
 CC -!- FUNCTION: Orphan receptor.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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 CC
 CC EMBL; AJ505757; CAD44281.1; --
 CC Genew; HGNC:4481; GPR26.
 CC MIM; 604847; --
 CC InterPro; IPR000276; GPCR_Rhodpsn.
 CC Pfam; PF00001; 7tm 1; 1.
 CC PRINTS; PRO0237; GPCRHOOPS.
 CC PROSITE; PS00237; G-PROTEIN RECEPTOR F1.1; FALSE_NEG.
 CC PROSITE; PS00262; G-PROTEIN RECEPTOR F1.2; 1.
 KW G-protein coupled receptor; Transmembrane.
 FT DOMAIN 1 10
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 11 31
 FT CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 32 47
 FT DOMAIN 48 68
 FT TRANSMEM 69 81
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 82 102
 FT DOMAIN 103 123
 FT CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 124 144
 FT DOMAIN 145 168
 FT TRANSMEM 169 189
 FT CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 190 245
 FT DOMAIN 246 266
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 267 276
 FT CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 277 297
 FT DOMAIN 298 337
 FT DISULFID 79 156
 BY SIMILARITY.
 SQ SEQUENCE 337 AA; 37603 MW; 4E04D371505F6D01 CRC64;

Query Match 45.6%; Score 848; DB 1; Length 337;
 Best Local Similarity 52.0%; Pred. No. 3.8e-56;
 Matches 170; Conservative 52; Mismatches 101; Indels 4; Gaps 1;

QY 1 MGPGALLAGLLVMVLAVALLSNALVLLCCAYSSELTRASGVLLVNLGLHLLAALDM 60
 DB 1 MNSWDAGLAGLVGTNGVSLVNLVLLCLHSADIRQAPALFTLTCGNLLCTVNM 60
 QY 61 PFTLLGVNRGRTSPAPGACQVIGFLDTFLASNAALSVAALSADQWLAVGPFPLRYAGRLRP 120
 DB 61 PLTLAGVVAQRQPGADRLCLAAFLDTFLAANSMLSMALSIDRWVAVVFLSYRAKWL 120
 QY 121 RYAGLLGCAGQSLAFSGAALGCSWLGYSAPFASCSLRLPPEPRPFAATLHVG 180
 DB 121 RDAALMVAVTWLHALTFPAALALSWLGFHQIYASCTICSSRRPDELRLFAVTFGFAHLS 180
 QY 181 FVLPLAVLCLSLQVHRVARHCQRMDDVTVMKALAVLADLHPSVRCGLIQKKRRHRAT 240

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Db 181 FLLSFVLCCTVLLKLVARFCKRIDVTMTQTLVLLDLHPSVERCLESEKRRQRAT 240
QY 241 RKIGIAIATFLICFAPYVMTLAEVFPVTVNAQNGILSKCLTYSKAVADPTYSLLRRP 300
Db 241 KKISTIFGFLVCFAPYVITRLVELFSTVPIGSHGVLSKCLAYSKAASDPFVYSLRHQ 300
QY 301 FRQVLGAVHRLKRTPRPASTHDSLSL 327
Db 301 YRSCKEILNRLHR-----RSIHSSGL 323

RESULT 3
GP26 RAT STANDARD; PRT; 337 AA.
AC Q9QXI3;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DE Probable G protein-coupled receptor GPR26.
GN GPR26.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=20149952; PubMed=10684976;
RA Lee D.K., Lynch K.R., Nguyen T., Im D.-S., Cheng R., Saldivia V.R.,
RA Liu Y., Liu I.S.C., Heng H.H.Q., Seeman P., George S.R., O'Dowd B.F.,
RA Marchese A.;
RT "Cloning and characterization of additional members of the G protein-
coupled receptor family."
RL Biochim. Biophys. Acta 1490:311-323 (2000).
CC -!- FUNCTION: Orphan receptor.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Detected in extracts of several brain regions
including striatum, pons, cerebellum and cortex. Not detected in
numerous peripheral tissue extracts, except in testis. In the
brain, detected in cortical structures including the anterior
cingulate area, posterior cingulate and the frontoparietal,
somatosensory and piriform cortices. Prominent also in the
olfactory tubercle, the islands of Calleja, ventromedial and
posterior nuclei of the hypothalamus, the medial septal nucleus,
nucleus of the diagonal band and the ventral tegmental area.
Localized also to hippocampal structures, with signals strongest
over the CA2 and CA3 regions of Ammon's horn and less so over the
dentate gyrus. Expressed in the caudate putamen only in its most
caudal portion, with a decreasing gradient of signal from the
dorsal to ventral aspect. Strong expression associated with a
single pontine structure, the inferior olivary nucleus.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF208288; AAF21012.1; -.
CC InterPro: IPR000276; GPCR Rhodopsin.
CC InterPro: IPR000169; SHprot_acsite.
CC Pfam: PF00001; 7tm1.1; 1.
CC PRINTS; PR00237; GPCRHHODPSN.
CC PROSITE; PS00237; G PROTEIN RECEPTOR FL1; FALSE_NEG.
CC PROSITE; PS0262; G PROTEIN RECEPTOR FL2; 1.
CC G-protein coupled receptor; Transmembrane.
KW DOMAIN 1 10 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 11 31 1 (POTENTIAL).
FT DOMAIN 32 47 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 48 68 2 (POTENTIAL).

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FT DOMAIN 69 81 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 82 102 3 (POTENTIAL).
FT DOMAIN 103 123 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 124 144 4 (POTENTIAL).
FT DOMAIN 145 168 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 169 189 5 (POTENTIAL).
FT DOMAIN 190 245 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 246 266 6 (POTENTIAL).
FT DOMAIN 267 276 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 277 297 7 (POTENTIAL).
FT DOMAIN 298 337 CYTOPLASMIC (POTENTIAL).
FT DISULFID 79 156 BY SIMILARITY.
SQ SEQUENCE 337 AA; 37804 MW; CD7E2381F085F2DD CRC64;

Query Match 44.3%; Score 823; DB 1; Length 337;
Best Local Similarity 49.1%; Pred No. 2.7e-54;
Matches 164; Conservative 58; Mismatches 106; Indels 6; Gaps 2;

QY 1 MGCEALLAGLVMLVLAVALLSNALVLLCCYSAELRTRASGVLLVNLGHLALLAALDM 60
Db 1 MNSWDAGLAGLVGTIGVLSLLSNGLLVLLCLLHSDIRROQAPALFTLMLTCGNLLCTVVM 60
QY 61 PFTLLGVRGRTSPAGCAQVIGFLDTFLASNAALSVAALSADQWLAVGFLPAGRLRP 120
Db 61 PTLTAGVVAQRQAPAGDRCLRLAFLDTFLAANSLNSAALSIDRWVAVPFLSYRAQRL 120
QY 121 RYAGLLGCAGGOSLAFSGAALGCSMLGYSSAFASCSRLRPPERPRFAATATLHVG 180
Db 121 RDAAFVAVYTWLHALTPATALALSMLGPHQLYASCTLCRRPDERLRFVFTSAPHALS 180
QY 181 FVLPLAVLCITSQVHRVARRHQMDVTMKALALLADLHPSVQRCLQOKRRHRAT 240
Db 181 FLSFVLCFTYLKLVKVARFCHKRIDVTMTQTLVLLDLHPSVRECLSEQKRRQRAT 240
QY 241 RKIGIAIATFLICFAPYVMTLAEVFPVTVNAQNGILSKCLTYSKAVADPTYSLLRRP 300
Db 241 KKISTIFGFLVCFAPYVITRLVELFSTVPIGSHGVLSKCLAYSKAASDPFVYSLRHQ 300
QY 301 FRQVLGAVHRLKRTPRPASTHDSLSL 334
Db 301 YRSCKEILNRLHR-----RSIH--SVGLTGDSH 328

RESULT 4
GP26 MOUSE STANDARD; PRT; 337 AA.
AC Q8BZA7; Q80T55; Q8BXZ5;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Probable G protein-coupled receptor GPR26.
GN GPR26.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=CS7BL/6J; TISSUE=Cerebellum;
RX MEDLINE=22354683; PubMed=12466851;
RA Okazaki Y., Furuno M., Kasukawa T., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Nikaigo I., Osato N., Saito K., Hume D.A., Quackenbush J.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Batalov S., Beisel K.W.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Cousins S.,
RA Blake J.A., Bradt D., Brusci V., Ciothia C., Corbani L.B., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,

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RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Vardaro R., Wagner L., Wallestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imocani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sakai D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.,
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573 (2002).
RN [2]
RP SEQUENCE OF 117-291 FROM N.A.
RX MEDLINE=22584407; PubMed=12679517;
RA Vassiliadis D.K., Hohmann J.G., Zeng H., Li F., Ranchalis J.E.,
RA Mortrud M.T., Brown A., Rodriguez S.S., Weller J.R., Wright A.C.,
RA Bergmann J.E., Gaitanaris G.A.;
RT "The G-protein-coupled receptor repertoire of human and mouse.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:4903-4908 (2003).
CC -!- FUNCTION: Orphan receptor.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Exclusively expressed in the brain.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL; AK036100; BAC29305.1; -;
DR EMBL; AK042755; BAC31354.1; -;
DR EMBL; AY255585; AA085097.1; -;
DR MGD; MGI:2441758; Gpr26.
DR InterPro; IPR000169; GPCR_Rhodopsin.
DR InterPro; IPR000169; SHPOT_acsite.
DR Pfam; PF00001; 7tm1.1;
DR PRINTS; PR00237; GPCR_Rhodopsin.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; FALSE_NEG.
DR PROSITE; PS00262; G-PROTEIN RECEPTOR FL2; 1.
KW G-protein coupled receptor; Transmembrane.
FT DOMAIN 1 10
FT TRANSMEM 11 31
FT DOMAIN 32 47
FT TRANSMEM 48 68
FT DOMAIN 69 81
FT TRANSMEM 82 102
FT DOMAIN 103 123
FT TRANSMEM 124 144
FT DOMAIN 145 168
FT TRANSMEM 169 189
FT DOMAIN 190 245
FT TRANSMEM 246 266
FT DOMAIN 267 276
FT TRANSMEM 277 297
FT DOMAIN 298 337
FT TRANSMEM 338 357
FT DISULFID 79 156
FT CONFLICT 156 156
SQ SEQUENCE 337 AA; 37746 MW; CDYCF1544E722DD CRC64;
Query Match 44.2%; Score 822; DB 1; Length 337;
Best Local Similarity 49.1%; Pred. No. 3.3e-54;
Matches 164; Conservative 57; Mismatches 107; Indels 6; Gaps 2;
QY 1 MCGPAGALLAGLVVAVLALSNALVLCAYSAELRTRASGVLLVNLGLHLLAALDM 60

Db 1 MNSWDAGLGLLVGTIGVYLLSNGLVLLCLLHSDADIRQAPALFTLNTCGNLLCTVVM 60
QY 61 PPTLLGVNRGTPSPAGCAQVIGLDTFLASNAALSAALSDADQWLAQVGLPVRGR 120
Db 61 PPTLLGVNRGTPSPAGCAQVIGLDTFLASNAALSAALSDADQWLAQVGLPVRGR 120
QY 121 RVAGLLGCAWQSLAFSGAALGCSWLGYSFAFASCSRLPPEPRPFAAFTATLHVG 180
Db 121 RDAAPWAVYTWLHALTFPATLALSWLGHQLYASCTLCSSRRPDERLFAVTSFAHLS 180
QY 181 FVLPLAVLCLTSQVHRVARHCQMDVTWKALLADLHPSVQRCLIOQKRREHAT 240
Db 181 FLSFVLVLCFTYLVKLVARFHCGRIDVTQTLVLLVDIHPSVRERCEBQKRQRAT 240
QY 241 RKIGIAITAFICFAPYVYMTLAEVPPVTNAQWGLSKCLTYSKAVADFTYLLRRP 300
Db 241 KKISTFGLTFLVCFAPYVITRIVELFSTAPIGSHGVLSKCLAYSKAASDFVYSLLRHQ 300
QY 301 FQVLGAMVHRLKTRTPASTHSSLDVAGNVH 334
Db 301 YRRCKELNRIENR---RSLH--SVGLTGDSH 328
RESULT 5
SH6_MOUSE STANDARD; PRT; 440 AA.
AC Q9RIC8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 5-hydroxytryptamine 6 receptor (5-HT-6) (Serotonin receptor).
GN HTR6.
OC Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ; TISSUE=Brain;
RX MEDLINE=21290977; PubMed=11406289;
RA Kohen R., Fashingbauer L.A., Heidmann D.E.A., Guthrie C.R.,
RA Hamblin M.W.;
RT "Cloning of the mouse 5-HT6 serotonin receptor and mutagenesis
RT studies of the third cytoplasmic loop.";
RL Brain Res. Mol. Brain Res. 90:110-117 (2001).
CC -!- FUNCTION: THIS IS ONE OF THE SEVERAL DIFFERENT RECEPTORS FOR 5-
CC HYDROXYTRYPTAMINE (SEROTONIN), A BIOGENIC HORMONE THAT FUNCTIONS AS
CC A NEUROTRANSMITTER, A HORMONE, AND A MITOGEN. THE ACTIVITY OF THIS
CC RECEPTOR IS MEDIATED BY G PROTEINS THAT STIMULATES ADENYLATE
CC CYCLASE. IT HAS A HIGH AFFINITY FOR TRICYCLIC PSYCHOTROPIC DRUGS
CC (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF134158; AAD46490.1; -;
DR MGD; MGI:1196627; Htr6.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm1.1;
DR PRINTS; PR00237; GPCR_Rhodopsin.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; 1.
DR PROSITE; PS00262; G-PROTEIN RECEPTOR FL2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family.
FT DOMAIN 1 34
FT TRANSMEM 35 57
FT EXTRACELLULAR (POTENTIAL).
FT 1 (POTENTIAL).

FT DOMAIN 58 64 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 65 85 2 (POTENTIAL).
FT DOMAIN 86 100 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 101 122 3 (POTENTIAL).
FT DOMAIN 123 144 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 145 166 4 (POTENTIAL).
FT DOMAIN 167 184 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 185 208 5 (POTENTIAL).
FT DOMAIN 209 267 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 268 292 6 (POTENTIAL).
FT DOMAIN 293 297 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 298 322 7 (POTENTIAL).
FT DOMAIN 323 440 CYTOPLASMIC (POTENTIAL).
FT DISULFID 99 180 BY SIMILARITY.
FT CARBOHYD 3 9 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 440 AA; 46998 MW; 4440CDEB01FEF0C CRC64;

Query Match 13.2%; Score 245.5; DB 1; Length 440;
Best Local Similarity 25.1%; Pred. No. 3e-11;
Matches 100; Conservative 68; Mismatches 174; Indels 57; Gaps 15;

QY 2 GPGEA-----LLAGLLVMVLAALLSNALVLLCCAYSABLRTASGVLLVNLGLH 53
DB 16 GPGEPPAPGSGWVAALCVVLTAAANSLTALICTOPALRNT--SNFFLVSLTSDL 73

QY 54 LLAALDMPFTLLGVMRGTPSAPGACQVIGFDTFLASNAALSVAALSADQWLVGFPLR 113
DB 74 MVGLVWPAMPALNLYGRVWLGCLLTWAFVWCCSASILNCLISLDYVLLLSPLR 133

QY 114 YAGRL-RPYAGLLIGCANGOSIA-----FSGAALGCSWLG--YSSAFACSL--RLPPEP 164
DB 134 YKRLMTAPRALILG-AW--SLAALASFLPLLLGHWELGKARTAPGQCRLIASLP--- 187

QY 165 ERPRFAAFTATLHAGVFLPLVLCVLTSLQVHVARHQRQMDTVT-----MKALA 215
DB 188 -----YVVASGVTFPLPSGACFTYCYRILLARKQAVASLTGTATAGQALETLQ 240

QY 216 LLAHLHPSVR----QRCLIQKRRHRKRGIAIAITFLICPAPVMTRIAELVPFVTV 271
DB 241 VPRTPRPGMESADSRLLTKHKKALKASLTIGLLSMFVFWLFFVFAVIAQAQVDCIS 300

QY 272 NAQWGLSKCLTYSKAVADPFYSLRRPFRVLAGWV-----HRLKRTPRPASTH 323
DB 301 PGLFDVLT-WLGCNSTWPIYPLFMRDFKALGRFVFCVCPPEHRASPASPSWTS 359

QY 324 DSSLVAGMVHQLKRTPRPASTHNGSVDTENDSCLQOT 362
DB 360 SGAR--PGLSLQVQLPLPLPPNSDSDSA--SGGTSGQLQT 395

RESULT 6
SH6 HUMAN STANDARD; PRT; 440 AA.
AC P50406; Q13640;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE 5-hydroxytryptamine 6 receptor (5-HT-6) (Serotonin receptor).
GN HTR6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RT TISSUE=Striatum;
RC MEDLINE=96102917; PubMed=8522988;
RA Kohen R., Metcalf M.A., Khan N., Druck T., Huebner K., Lachowicz J.E.,
RA Sibley D.R., Roth B., Hamblin M.W.;
RT "Cloning, characterization, and chromosomal localization of a human
RT 5-HT6 serotonin receptor";
RL J. Neurochem. 66:47-56 (1996).
RN [2]

RP SEQUENCE OF 215-280 FROM N.A.
RC TISSUE=Striatum;
RX MEDLINE=95385798; PubMed=7656980;
RA Ullmer C., Schmuck K., Kalkman H.O., Lubbert H.;
RT "Expression of serotonin receptor mRNAs in blood vessels.";
RL FEBS Lett. 370:215-221 (1995).
CC -I- FUNCTION: This is one of the several different receptors for 5-hydroxytryptamine (serotonin), a biogenic hormone that functions as a neurotransmitter, a hormone, and a mitogen. The activity of this receptor is mediated by G proteins that stimulates adenylate cyclase. It has a high affinity for tricyclic psychotropic drugs.
CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
CC -I- TISSUE SPECIFICITY: Expressed in several human brain regions, most prominently in the caudate nucleus.
CC -I- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
DR EMBL; L41147; AAA92622.1; -.
DR EMBL; Z49119; CA88929.1; -.
DR PIR; JC5520; JCS520.
DR Genew; HGNC:5301; HTR6.
DR MIM; 601109; -.
DR GO; GO:0005887; C: integral to plasma membrane; TAS.
DR GO; GO:004989; P: histamine receptor activity; TAS.
DR GO; GO:0007187; P: G-protein signaling, coupled to cyclic nucl. .; TAS.
DR GO; GO:0007268; P: synaptic transmission; TAS.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F2_1; 1.
DR KW G-protein coupled receptor; Transmembrane; Glycoprotein; Multigene family.
FT DOMAIN 1 34 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 35 57 1 (POTENTIAL).
FT DOMAIN 58 64 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 65 85 2 (POTENTIAL).
FT DOMAIN 86 100 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 101 122 3 (POTENTIAL).
FT DOMAIN 123 144 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 145 166 4 (POTENTIAL).
FT DOMAIN 167 184 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 185 208 5 (POTENTIAL).
FT DOMAIN 209 265 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 266 290 6 (POTENTIAL).
FT DOMAIN 291 295 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 296 320 7 (POTENTIAL).
FT DOMAIN 321 440 CYTOPLASMIC (POTENTIAL).
FT DISULFID 99 180 BY SIMILARITY.
FT CONFLICT 247 247 V -> M (IN REF. 2).
SQ SEQUENCE 440 AA; 46954 MW; C888F47650C1D2EF CRC64;

Query Match 13.2%; Score 244.5; DB 1; Length 440;
Best Local Similarity 26.1%; Pred. No. 3.6e-11;
Matches 102; Conservative 64; Mismatches 164; Indels 61; Gaps 17;

QY 2 GP-----GEALLAGLLVMVLAALLSNALVLLCCAYSABLRTASGVLLVNLGLHLL 55
DB 18 GPSPAPGSGWVAALCVVLTAAANSLTALICTOPALRNT--SNFFLVSLTSDLMV 75

QY 56 AALDMPFTLLGVMRGTPSAPGACQVIGFDTFLASNAALSVAALSADQWLVGFPLRYA 115
DB 76 GLVWVWPAMPALNLYGRVWLGCLLTWAFVWCCSASILNCLISLDYVLLLSPLRYK 135

QY 116 GLRPP-RYAGLLIGCANGOSIA-----FSGAALGCSWLGYSASFASCSLRPPPRPFA 170
RN [2]

Db 136 LMTFRLALVLG-AW--SIAALASFLPLLGHHELGHAR-----PPVPGQCRLL 183
 Qy 171 A---FTATLHVGFLVPLAVLCLSLQVHRVARRHCOEMDTVT-----MKALLALLADL 220
 Db 184 ASLPVVLVASGLTFLPSGAICFTYCRILLARQAVQVSLTTGMSAQASSETLQVPTP 243
 Qy 221 HPSVR-----QRCLQOKRRRHARKIGIATATFLICFAPVYVTRLAEPLVFFVTVNAQWG 276
 Db 244 RGVESADSRRLATKHSKALKASLTGLLGMFFVTWLPFFVANIYVQAVCDICSPGLFD 303
 Qy 277 ILKCLITYSKAVADFTYSLLRPRPQVLAGVHRL--KTP--RPASTHDSLDVA-- 330
 Db 304 VLT-WLGCNSMNPILYPLFPROFKALG-----RFLPCPCPRQASLASPSLRSHS 358
 Qy 331 ----GMVQLLKRTPRPASTNGSVDTENDS 357
 Db 359 GPRGLSLQVVLPLPLP-----DSDSDS 382

RESULT 7
 SSR4 HUMAN
 ID SSR4_HUMAN STANDARD; PRT; 388 AA.
 AC P31391; Q9UUY1;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Somatostatin receptor type 4 (SS4R).
 GN SSR4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 ON NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93290656; PubMed=8512564;
 RA Xu Y., Song J., Bruno J.F., Berelowitz M.;
 RT "Molecular cloning and sequencing of a human somatostatin receptor,
 RT hSSR4.";
 RL Biochem. Biophys. Res. Commun. 193:648-652(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93249256; PubMed=8483934;
 RA Rohrer L., Raulf F., Bruns C., Buettner R., Hofstaedter F.,
 RA Schuele R.;
 RT "Cloning and characterization of a fourth human somatostatin
 RT receptor.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:4196-4200(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93384611; PubMed=8373420;
 RA Yamada Y., Kagimoto S., Kubota A., Yasuda K., Masuda K., Someya Y.,
 RA Ihara Y., Li Q., Imura H., Seino S., Seino Y.;
 RT "Cloning, functional expression and pharmacological characterization
 RT of a fourth (hSSR4) and a fifth (hSSR5) human somatostatin receptor
 RT subtype.";
 RL Biochem. Biophys. Res. Commun. 195:844-852(1993).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93302729; PubMed=8100352;
 RA Demchyshyn L.L., Srikant C.B., Sunahara R.K., Kent G., Seeman P.,
 RA van Tol H.H.M., Panetta R., Patel Y.C., Niznik H.B.;
 RT "Cloning and expression of a human somatostatin-14-selective receptor
 RT variant (somatostatin receptor 4) located on chromosome 20.";
 RL Mol. Pharmacol. 43:894-901(1993).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21638749; PubMed=11780052;
 RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
 RA Jones M., Stavrides G., Alnida J.P., Babbage A.K., Bagguley C.L.,
 RA Bailey J., Barlow K.P., Bates K.N., Beard L.M., Beare D.M., Brown A.J.,
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
 RA Chapman J.C., Clamp M., Clark M., Clark L.N., Clark S.Y., Clee C.M.,

Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
 Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
 Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 Leheslahti M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 Marsh V.I., Martin S.I., McConachie L.J., McLeay K., McMurray A.,
 Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
 Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkneen R., Sims S.,
 Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
 Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M., Williams S.A.,
 Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
 Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 20.";
 RL Nature 414:865-871(2001).
 CC -1- FUNCTION: Receptor for somatostatin-14. The activity of this
 CC receptor is mediated by G proteins which inhibits adenylyl
 CC cyclase. It is functionally coupled not only to inhibition of
 CC adenylate cyclase, but also to activation of both arachidonate
 CC release and mitogen-activated protein (MAP) kinase cascade.
 CC Mediates antiproliferative action of somatostatin in tumor cells.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Specifically expressed in fetal and adult
 CC brain, lung tissue, stomach, and in lesser quantities in the
 CC kidney, pituitary and adrenals.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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 CC
 CC EMBL: D16826; BAA04106.1; -;
 CC EMBL: L14856; AAA36623.1; -;
 CC EMBL: L07833; AAA60565.1; -;
 CC EMBL: L07061; -; NOT ANNOTATED CDS.
 CC EMBL: AL049651; CAB51953.1; -;
 CC PIR: JN0605; JN0605.
 CC HSP: P02699; IBOJ.
 CC Genew: HGNC:11333; SSTR4.
 CC MIM: 182454; -;
 CC GO: GO:0003887; C:integral to plasma membrane; TAS.
 CC GO: GO:0004994; F:somatostatin receptor activity; TAS.
 CC GO: GO:0007187; P:G-protein signaling, coupled to cyclic nucl.; TAS.
 CC GO: GO:0008285; P:negative regulation of cell proliferation; TAS.
 CC InterPro: IPR000276; GPCR_rhodpsn.
 CC Pfam: PF00001; 7tm.1.1.
 CC PRINTS: PR00237; GPCRHOPOSN.
 CC PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
 CC PROSITE: PS00262; G_PROTEIN_RECEP_F1_2; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein;
 CC Multigene family; Lipoprotein; Palmitate; Phosphorylation;
 CC Polymorphism.
 CC DOMAIN 1 46 EXTRACELLULAR (POTENTIAL).
 CC TRANSSEM 47 73 1 (POTENTIAL).
 CC DOMAIN 74 83 CYTOPLASMIC (POTENTIAL).
 CC TRANSSEM 84 104 2 (POTENTIAL).
 CC DOMAIN 105 120 EXTRACELLULAR (POTENTIAL).
 CC TRANSSEM 121 142 3 (POTENTIAL).
 CC DOMAIN 143 161 CYTOPLASMIC (POTENTIAL).
 CC TRANSSEM 162 185 4 (POTENTIAL).
 CC DOMAIN 186 208 EXTRACELLULAR (POTENTIAL).
 CC TRANSSEM 209 232 5 (POTENTIAL).
 CC DOMAIN 233 260 CYTOPLASMIC (POTENTIAL).

FT	TRANSMEM	261	280	6 (POTENTIAL).
FT	DOMAIN	281	291	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	292	314	7 (POTENTIAL).
FT	DOMAIN	315	388	CYTOPLASMIC (POTENTIAL).
FT	CARBOHYD	24	24	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	DILIPID	119	198	BY SIMILARITY.
FT	LIPID	327	327	S-palmitoyl cysteine (Potential).
FT	VARIANT	83	83	N-> T (in dSNP:1065191).
FT	CONFLICT	284	284	/FTID=VAR_011703.
FT	CONFLICT	321	321	V -> F (IN REF. 4 AND 5).
FT	CONFLICT	365	365	S -> F (IN REF. 5).
FT	CONFLICT	365	365	P -> K (IN REF. 2).
SEQ	SEQUENCE	388 AA;	41894 MW;	8BCDD69B5F3BC2F5 CRC64;

Query Match	13.1%;	Score	243.5;	DB	1;	Length	388;
Best Local Similarity	25.5%;	Pred.	No. 3.8e-11;				
Matches	84;	Conservative	55;	Mismatches	124;	Indels	67;
						Gaps	10;

QY	2	GPGEALLAGLL	-----	VWMLAVALLSNALVLLCCAYSAELTRASGVLLNLSLGLL	55
DB <td>38</td> <td>GGGDARAGVAIQIYALVCLVGLGNALVIFILRYAKMT</td> <td>-----</td> <td>ATNIYLLNLVADELF</td> <td>96</td>	38	GGGDARAGVAIQIYALVCLVGLGNALVIFILRYAKMT	-----	ATNIYLLNLVADELF	96
QY <td>56</td> <td>AALDNPFLLGVMRGRTSPAGCAQVIGFLDTFLASNAUSVAALSADOWLAVGFLRYA</td> <td>115</td> <td></td> <td></td>	56	AALDNPFLLGVMRGRTSPAGCAQVIGFLDTFLASNAUSVAALSADOWLAVGFLRYA	115		
DB <td>97</td> <td>MLSVFPFVASSAALRHPFGSVLCRAVLSVDGLNMTSFVCLTVLSVDRYAVVHPLRAA</td> <td>155</td> <td></td> <td></td>	97	MLSVFPFVASSAALRHPFGSVLCRAVLSVDGLNMTSFVCLTVLSVDRYAVVHPLRAA	155		
QY <td>116</td> <td>GRLRPRYAGLLGCAGQSL</td> <td>-----</td> <td>AFSGAALGCS--WLGYSAFASCSLR</td> <td>159</td>	116	GRLRPRYAGLLGCAGQSL	-----	AFSGAALGCS--WLGYSAFASCSLR	159
DB <td>156</td> <td>TYRRSVAKLNLGWLASLVTPIAFADTRPARGQAVANLQW</td> <td>-----</td> <td></td> <td>202</td>	156	TYRRSVAKLNLGWLASLVTPIAFADTRPARGQAVANLQW	-----		202
QY <td>160</td> <td>LPPEPERPFAAFTATLHAGVFLPLAVLCITLSQVHRVARRHCORMDVTVMKALLAD</td> <td>219</td> <td></td> <td></td>	160	LPPEPERPFAAFTATLHAGVFLPLAVLCITLSQVHRVARRHCORMDVTVMKALLAD	219		
DB <td>203</td> <td>----PHPAWSAVFVVYTFLLGFLPLVAIGL</td> <td>-----</td> <td>CYLLIVGKRAVALRAG</td> <td>246</td>	203	----PHPAWSAVFVVYTFLLGFLPLVAIGL	-----	CYLLIVGKRAVALRAG	246
QY <td>220</td> <td>LHPSVQRCLQKERRHRAFKIGIAIAFLICFAPYVMTRIAELAVFPVTYNAQWGLIS</td> <td>279</td> <td></td> <td></td>	220	LHPSVQRCLQKERRHRAFKIGIAIAFLICFAPYVMTRIAELAVFPVTYNAQWGLIS	279		
DB <td>247</td> <td>WQ-----QRRSEKKITRLVMVWVVFVLCWMPFFYVVQQLNLV</td> <td>-----</td> <td>VTSLDATVNVHS</td> <td>296</td>	247	WQ-----QRRSEKKITRLVMVWVVFVLCWMPFFYVVQQLNLV	-----	VTSLDATVNVHS	296
QY <td>280</td> <td>KCLTYSKAVADPFTYSLL</td> <td>-----</td> <td>RRPFRQVL</td> <td>305</td>	280	KCLTYSKAVADPFTYSLL	-----	RRPFRQVL	305
DB <td>297</td> <td>LILSVANSKANPILYGFLSDNFRSFQRL</td> <td>326</td> <td></td> <td></td>	297	LILSVANSKANPILYGFLSDNFRSFQRL	326		

RESULT 8	SH6_RAT	SH6_RAT	STANDARD;	PRT;	436 AA.
ID	AC	P31388;			
DT	01-JUL-1993	(Rel. 26, Created)			
DT	01-NOV-1995	(Rel. 32, Last sequence update)			
DT	15-DEC-1998	(Rel. 37, Last annotation update)			
DE	5-hydroxytryptamine 6 receptor (5-HT-6) (Serotonin receptor)	(ST-B17).			
GN	HTR6.				
OS	Rattus norvegicus (Rat).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				
OX	NCBI_Taxid:10116;				
[1]	SEQUENCE FROM N.A.				
RP	STRAIN=Sprague-Dawley; TISSUE=Striatum;				
RC	MEDLINE=93196608; PubMed=7680751;				
RA	Monsma F.J., Jr., Shen Y., Ward R.P., Hamblin M.W., Sibley D.R.;				
RT	"Cloning and expression of a novel serotonin receptor with high				
RT	affinity for tricyclic psychotropic drugs.";				
RL	Mol. Pharmacol. 43:320-327(1993).				
[2]	SEQUENCE FROM N.A.				
RP	MEDLINE=93277562; PubMed=8389146;				
RA	Ruat M., Traiffort E., Arrang J.-M., Tardivel-Lacombe J., Diaz J.,				
RA	Leurs R., Schwartz J.-C.;				
RT	"A novel rat serotonin (5-HT6) receptor: molecular cloning,				
RT	localization and stimulation of cAMP accumulation.";				
RL	Biochem. Biophys. Res. Commun. 193:268-276(1993).				

QY 114 YAGRL-RPYAGLLGCAWGSLA----FSGAALGCSWLGSSAFASCSRLRLPEPERPR 168
 DB 134 YKLRWAPRALALIG-AW-SLAALASFLPLLLGWLHGLKART-----PAGQCR 181
 QY 169 FAA---FATLHAGVFLPLAVCLTSLQVHRVARRHCQMDVT-----MKALALLA 218
 DB 182 LLASLPFLVAGSVTFPLPSGAICFTYCRILLARKQAVQVASTTGTAGQALLETQVPR 241
 QY 219 DLHESVR---ORCLIQKRHRHATRKIGIAITATFICFAPYVWTRIALSLVPFTVNAQ 274
 DB 242 TPRMESADSRRLATHSRKALKASUTGLILLGNFFVFWLPPFVANIAQVCDICSPGL 301
 QY 275 WGIILSKLTYSKAVADPFTYSLRRPQVL 305
 DB 302 FDLVT-WLGYCNSTWNPPIIYPLFNRDFKRAL 331

RESULT 9
 HH2R_CAVPO STANDARD; PRT; 359 AA.
 AC P47747;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Histamine H2 receptor (H2R) (Gastric receptor I).
 GN HR42.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
 OX NCBI_TaxID=10141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Hartley; TISSUE=Liver;
 RA Traifort E.;
 RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: The H2 subclass of histamine receptors mediates gastric acid secretion. The activity of this receptor is mediated by G proteins which activate adenylyl cyclase.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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 CC
 CC EMBL; U25440; AAA65713.1; -.
 DR PIR; JC4120; JC4120.
 DR HSP; P29274; LMWH.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm1.1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Lipoprotein; Palmitate.
 FT DOMAIN 1 22 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 23 44 1 (POTENTIAL).
 FT DOMAIN 45 57 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 58 81 2 (POTENTIAL).
 FT DOMAIN 82 92 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 93 114 3 (POTENTIAL).
 FT DOMAIN 115 134 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 135 159 4 (POTENTIAL).
 FT DOMAIN 160 180 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 181 204 5 (POTENTIAL).
 FT DOMAIN 205 234 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 235 258 6 (POTENTIAL).
 FT DOMAIN 259 267 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 268 289 7 (POTENTIAL).
 FT DOMAIN 290 359 CYTOPLASMIC (POTENTIAL).
 FT SITE 98 ESSENTIAL FOR HISTAMINE BINDING (BY SIMILARITY).
 FT SITE 186 ESSENTIAL FOR TIOTIDINE BINDING AND IMPLICATED IN HISTAMINE BINDING (BY SIMILARITY).
 FT SITE 190 IMPLICATED IN HISTAMINE BINDING (BY SIMILARITY).
 FT LIPID 305 305 S-palmitoyl cysteine (By similarity).
 FT CARBOHYD 4 4 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT DISULFID 91 174 BY SIMILARITY.
 SQ SEQUENCE 359 AA; 40556 MW; 58DB81BD8FC3C0E9 CRC64;

Query Match 12.5%; Score 232.5; DB 1; Length 359;
 Best Local Similarity 22.0%; Pred. NO. 2.3e-10;
 Matches 73; Conservative 67; Mismatches 139; Indels 53; Gaps 8;

QY 11 LLVMVLAVALLSNALVLLCCAVSABLRTASGLVNLNLSGLHLLIAALDMEFTLLGVNRG 70
 DB 24 ILIILILVTAGVVVCLAVGLNRLRS-LTNCFIVSLAVTDLLGLLVLPFSAIYQLSC 82
 QY 71 RTPSAPGACQVIGFLDTFLASNAALSVLAASADQWLVGFFLYAGRURPRYAGLLGCA 130
 DB 83 KNSFSKVFNCNIYTSLDVMLCTASILNLFMISLDRYCAVTDELRYEVLITPARVAISLVFI 142
 QY 131 WQSIAFSGAALGCSWLGV-----SSAFASCSRLPEPERPFAATLHAGVFLP 184
 DB 143 WISITLSPFLSIHLGWSNRNETSKNDIVKCKGVN-----EVYGLVDGLVTFYLP 194
 QY 185 LAVLCUTSLQVHRVARRHCQMDTV-TMKALLADLHPSVQRCLIOCKRRRHATRKI 243
 DB 195 LLIMCITYFRIFKIAREQARRINHIGSWKAATI-----REHKATVTL 236
 QY 244 GIAIATFELICFAPYVWTRIAELVFPV-----TVNAQWGLSKLTYSKAVADPFTYS 295
 DB 237 AAVMGAFILCWFPY-----FTVFYRGLKGDADVNEFEDVVLWLGYSALNPILYA 289
 QY 296 LLRRPRFQVLWGVHRLKRTPRPASTHDSLSL 327
 DB 290 ALNRDPTA----YHQLFCCRLASHSHSETSL 317

RESULT 10
 SH4_MOUSE STANDARD; PRT; 388 AA.
 AC P97288; O89003; O89004; Q9R2A4;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE 5-hydroxytryptamine 4 receptor (5-HT4) (Serotonin receptor) (5-HT4).
 GN HTR4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Swiss; TISSUE=Brain;
 RX MEDLINE=97102706; PubMed=8946946;
 RA Claeysen S., Sebben M., Journot L., Bockaert J., Dumuis A.;
 RT "cloning, expression and pharmacology of the mouse 5-HT(4L) receptor".;
 RL FEBS Lett. 398:19-25 (1996).
 RN [2]
 RP REVISIONS TO C-TERMINUS.
 RA Dumuis A.;
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORMS 5-HT4(A) AND 5-HT4(E)).
 RC STRAIN=Swiss; TISSUE=Brain;
 RX MEDLINE=99127199; PubMed=9928238;
 RA Claeysen S., Paye P., Sebben M., Taviaux S., Bockaert J., Dumuis A.;

"5-HT4 receptors: cloning and expression of new splice variants."; Ann. N.Y. Acad. Sci. 861:49-56(1998).

[4]

SEQUENCE FROM N.A. (ISOFORM 5-HT4(F)).

TISSUE=Brain;

MEDLINE=99238795; PubMed=10205070;

Clayeyen S., Sebben M., Becamert C., Bockaert J., Dumuis A.;

"Novel brain-specific 5-HT4 receptor splice variants show marked constitutive activity: role of the C-terminal intracellular domain."; Mol. Pharmacol. 55:910-920(1999).

-!- FUNCTION: This is one of the several different receptors for 5-hydroxytryptamine (serotonin), a biogenic hormone that functions as a neurotransmitter, a hormone, and a mitogen. The activity of this receptor is mediated by G proteins that stimulates adenylyate cyclase (By similarity).

-!- SUBCELLULAR LOCATION: Integral membrane protein.

-!- ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=4;

Name=1;

IsoId=p97288-1; Sequence=Displayed;

Names=5-HT4(A);

IsoId=p97288-2; Sequence=VSP_001851;

Names=5-HT4(E);

IsoId=p97288-3; Sequence=VSP_001852;

Names=5-HT4(F);

IsoId=p97288-4; Sequence=VSP_001853;

-!- SIMILARITY: Belongs to family I of G-protein coupled receptors.

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EMBL; Y09585; CAA70773.1; --

DR DR EMBL; Y09587; CAA70775.1; --

EMBL; Y09588; CAA70776.1; --

DR DR EMBL; AJ011369; CAA09598.1; --

DR DR HSSP; P29274; 1MWH

DR DR MGD; MGI:109246; Htr4

DR DR InterPro; IPR000276; GPCR_Rhodopsn.

DR DR Pfam; PF00001; 7tm_1; 1.

DR DR PRINTS; PR00237; GPCRHHODOPS.

DR DR PROSITE; PS00237; G PROTEIN RECF F1_1; 1.

DR DR PROSITE; PS0262; G PROTEIN RECF F1_2; 1.

KH G-protein coupled receptor; Transmembrane; Glycoprotein;

KW Multigene family; Lipoprotein; Palmitate; Alternative splicing.

FT FT DOMAIN 1 19 EXTRACELLULAR (POTENTIAL).

FT FT TRANSMEM 20 40 1 (POTENTIAL).

FT FT DOMAIN 41 58 CYTOPLASMIC (POTENTIAL).

FT FT TRANSMEM 59 79 2 (POTENTIAL).

FT FT DOMAIN 80 93 EXTRACELLULAR (POTENTIAL).

FT FT TRANSMEM 94 116 3 (POTENTIAL).

FT FT DOMAIN 117 137 CYTOPLASMIC (POTENTIAL).

FT FT TRANSMEM 138 158 4 (POTENTIAL).

FT FT DOMAIN 159 192 EXTRACELLULAR (POTENTIAL).

FT FT TRANSMEM 193 213 5 (POTENTIAL).

FT FT DOMAIN 214 260 CYTOPLASMIC (POTENTIAL).

FT FT TRANSMEM 261 281 6 (POTENTIAL).

FT FT DOMAIN 282 294 7 (POTENTIAL).

FT FT TRANSMEM 295 315 EXTRACELLULAR (POTENTIAL).

FT FT DOMAIN 316 388 CYTOPLASMIC (POTENTIAL).

FT FT CARBOHYD 7 7 N-LINKED (GLCNAC...) (POTENTIAL).

FT FT DISULFID 93 184 BY SIMILARITY.

FT FT LIPID 329 329 S-palmitoyl cysteine (By similarity).

FT FT VARSPLIC 360 388 DAVECGGWESRCHLTATSPVLAAPSDDT -> YTVLHSGH HQEELXPIHNDPESLESCF (in isoform 5-HT4(A)).

FT FT VARSPLIC 359 388 /FTId=VSP_001851.

FT FT VARSPLIC 359 388 RDAVECGGWESRCHLTATSPVLAAPSDDT -> SPFLDLPF NRNPVY (in isoform 5-HT4(E)).

FT FT

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FT      VARSPLIC          360       388      /FTID=VSP_001852.  
FT      DAVECGQMSRCHLRTATSPLVAAPSDT -> PVPV (in  
FT      isoform 5-HT4(R)).  
FT      /FTID=VSP_001853.  
FT      SQ SEQUENCE      388 AA; 43931 MW; F84163F39BA115B0 CRC64;  
  
Query Match           12.5%; Score 232; DB 1; Length 388;  
Best Local Similarity 22.1%; Pred. No. 2.7e-10;  
Matches      89; Conservative 72; Mismatches 166; Indels 54; Gaps 10;  
  
QY    5 EALLAGLLVMVLAVALLSNALVLCCNYSAELTRASGVLLVNLSLGHLLAALDMPTLL 64  
      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
DB    19 KVVLLTFLLAVILMILGNLLVMVAVCRDLQRKIKTNFYIVSLAFADLLVSVLVMPFGA 78  
      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
QY    65 LGVMRGRTSPAGCAOVIGFLDTFLAGNAALSVAALSADOWLVGF-PLRYAGRLRPYA 123  
      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
DB    79 IEIVQDIWANGEFCLVRTSLDVLTLTASIFHLCCISLDRYAYACCPQVLYRNKWTPLRI 138  
      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
QY    124 GLILGCNWGQSLLAFSGAALCSW-----LGYSASFASCRLRLPPEPRPFA 170  
      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
DB    139 ALMLGGCWLPMTFSITFLPMQGNINIGVDVIEKRKFHSNSNTWCVMFW----NKP--- 191  
      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
QY    171 APTATLHVGFLVPLAVLCITSLQVHRVARRHQORMDTV-----TMKALALLADLHPSVR 225  
      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
DB    192 -YAITCSVAFYIPFLMVLAYRYIYVTAKEHAQQIQWLQAGATSSSRPOPADOHSTHR 250  
      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:~::~:  
QY    226 QRC LIQKRREHRAKTRKIGIALTFILCFAPYVYVTRLAEILVPFV--TVNAQWGILSKCLT 283  
      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
DB    251 M-----RRTKAAKTLCVIMGFCFCWAPPFFVTNIVD--PFIDYTVEQWTAFLWLG 301  
      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
QY    284 YSKAVADPPFTSYLLRRPFRQVLGWVHLLKRYTPRPASTDHSSLDVAGVHQLLKST-PR 342  
      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
DB    302 YINSLNPFLYAFNLKSFRALFIILCDDDERYKRP-----PILGQTVPVC 346  
      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
QY    343 PASTHNGSVDTEINDS 357  
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DB    347 STTINGSTHVLRDA 361  
      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
  
RESULT 11  
SSR5 HUMAN STANDARD; PRF; 364 AA.  
ID SSR5 HUMAN AC P3546; P34988; Q9UJ15;  
CT 01-JUN-1994 (Rel. 29, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Somatostatin receptor type 5 (SSSR).  
GN SSTR5.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI_Taxid=9606;  
[1]  
RN RFP SEQUENCE FROM N.A.  
RP MEDLINE=94195267; PubMed=7908405;  
RX Panetta R., Greenwood M.T., Wasyrnska A., Demchyshyn L.L., Day R.,  
RA Niznik H.B., Srikanth C.B., Patel Y.C.;  
RT "Molecular cloning, functional characterization, and chromosomal  
localization of a human somatostatin receptor (somatostatin receptor  
type 5) with preferential affinity for somatostatin-28.";  
RL Mol. Pharmacol. 45:417-427(1994).  
[2]  
RN RFP SEQUENCE FROM N.A.  
RP MEDLINE=93384611; PubMed=8373420;  
RX Yamada Y., Kagimoto S., Kubota A., Yasuda K., Masuda K., Someya Y.,  
RA Ihara Y., Li Q., Imura H., Seino S., Seino Y.;  
RT "Cloning, functional expression and pharmacological characterization  
of a fourth (hSSTR4) and a fifth (hSSTR5) human somatostatin receptor  
subtype".  
RL Biochem. Biophys. Res. Commun. 195:844-852(1993).  
[3]  
RN RFP SEQUENCE FROM N.A.  
RP MEDLINE=94359492; PubMed=8078491;  
RX
```

RA O'Carroll A.-M., Raynor K., Lolait S.J., Reisine T.;
 RT "Characterization of cloned human somatostatin receptor SSTR5.";
 RM Mol. Pharmacol. 46:291-298(1994).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21096910; PubMed=11157797;
 RA Daniels R.J., Peden J.F., Lloyd C., Horeley S.W., Clark K.,
 RA Tufarelli C., Kearney L., Buckle V.J., Doggett N.A., Flint J.,
 RA Higgins D.R.;
 RT "Sequence, structure and pathology of the fully annotated terminal 2
 RT MB of the short arm of human chromosome 16.";
 RL Hum. Mol. Genet. 10:339-352(2001).
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Baguley C.;
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Receptor for somatostatin 28 and to a lesser extent for
 CC somatostatin-14. The activity of this receptor is mediated by G
 CC proteins which inhibit adenylyl cyclase.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Adult pituitary gland, heart, small intestine,
 CC adrenal gland, cerebellum and fetal hypothalamus. No expression
 CC in fetal or adult kidney, liver, pancreas, uterus, spleen, lung,
 CC thyroid or ovary.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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 CC
 CC EMBL; L14865; AAA20828.1; -;
 CC EMBL; D16827; BAA04107.1; -;
 CC EMBL; AE006466; AAK61286.1; -;
 CC EMBL; AL031713; CAB56181.1; -;
 CC PIR; I57955; I57955.
 CC PIR; JN0763; JN0763.
 CC HSP; P02699; I988.
 CC Genew; HGNC:11334; SSTR5.
 CC MIM; 182455;
 CC GO; GO:0005887; C: integral to plasma membrane; TAS.
 CC GO; GO:0004994; P: somatostatin receptor activity; TAS.
 CC GO; GO:0007187; P: G-protein signaling, coupled to cyclic nucl. .; TAS.
 CC GO; GO:0008285; P: negative regulation of cell proliferation; TAS.
 CC InterPro; IPR000276; GPCR_Rhodopsin.
 CC Pfam; PF00001; 7tm.1; 1.
 CC PRINTS; PR00237; GPCR_Rhodopsin.
 CC PROSITE; PS00237; G-PROTEIN RECP_F1_1; 1.
 CC PROSITE; PS0262; G-PROTEIN RECP_F1_2; 1.
 CC KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 CC Multigene family; Lipoprotein; Palmitate; Phosphorylation.
 CC DOMAIN 1 38
 CC TRANSFAM 39 66
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RL FEBS Lett. 324:127-130(1993).
 RN [4]
 RP SEQUENCE OF 392-408 FROM N.A.
 RX MEDLINE=93125503; PubMed=1336117;
 RA Granneman J.G., Lahmans K.N., Rao D.D.;
 RT "rodent and human beta 3-adrenergic receptor genes contain an intron
 within the protein-coding block.";
 RL Mol. Pharmacol. 42:964-970(1992).
 RN [5]
 RP VARIANT ARG-64.
 RX MEDLINE=95334045; PubMed=7609752;
 RA Clement K., Vaisse C., Manning B.S.J., Basdevant A., Guy-Grand B.,
 Ruiz J., Silver K.D., Shuldiner A.R., Froquel P., Strosberg A.D.;
 RT "Genetic variation in the beta 3-adrenergic receptor and an increased
 capacity to gain weight in patients with morbid obesity.";
 RL New Engl. J. Med. 333:352-354(1995).
 RN [6]
 RP VARIANT ARG-64.
 RX MEDLINE=96361936; PubMed=8721782;
 RA Fujisawa T., Ikegami H., Yanato E., Takekawa K., Nakagawa Y.,
 Hamada Y., Oga T., Ueda H., Shintani M., Fukuda M., Ogiwara T.;
 RT "Association of Trp64Arg mutation of the beta3-adrenergic-receptor
 with NIDDM and body weight gain.";
 RL Diabetologia 39:349-352(1996).
 RN [7]
 RP VARIANT ARG-64.
 RX MEDLINE=96217306; PubMed=8641219;
 RA Candelore M.R., Deng L., Tota L.M., Kelly L.J., Cascieri M.A.,
 Strader C.D.;
 RT "Pharmacological characterization of a recently described human beta
 3-adrenergic receptor mutant.";
 RL Endocrinology 137:2638-2641(1996).
 RN [8]
 RP VARIANTS ARG-64 AND MET-265.
 RX MEDLINE=99318094; PubMed=10391210;
 RA Halushka M.K., Fan J.-B., Bentley K., Hsie L., Shen N., Weder A.,
 Cooper R., Lipshutz R., Chakravarti A.;
 RT "Patterns of single-nucleotide polymorphisms in candidate genes for
 blood-pressure homeostasis.";
 RL Nat. Genet. 22:239-247(1999).
 CC -!- FUNCTION: Beta-adrenergic receptors mediate the catecholamine-
 induced activation of adenylate cyclase through the action of G
 proteins. Beta-3 is involved in the regulation of lipolysis and
 thermogenesis.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Expressed mainly in adipose tissues.
 CC -!- POLYMORPHISM: The variant Arg-64 seems to be associated with
 weight gain (obesity) and to be also associated with
 susceptibility to non-insulin-dependent diabetes mellitus (NIDDM).
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -----
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 or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL; M29932; AAA35550.1; ALT_TERM.
 DR EMBL; X72861; CAA51383.1; -.
 DR EMBL; X70811; CAA50141.1; -.
 DR EMBL; X70812; CAA50142.1; ALT_SEQ.
 DR EMBL; X70812; CAA50143.1; ALT_SEQ.
 DR EMBL; S53291; AAB24837.1; -.
 DR PIR; I57941; I57941.
 DR PIR; S33751; ORHUBE.
 DR HSP; P29274; 1MWH.
 DR Genew; HGNC:288; ADRE3.
 DR MIM; 109691; -.
 DR GO; GO:0008887; C:integral to plasma membrane; TAS.
 DR GO; GO:0015052; F:beta3-adrenergic receptor activity; TAS.
 DR GO; GO:0005975; P:carbohydrate metabolism; TAS.

DR GO; GO:0006091; P:energy pathways; TAS.
 DR GO; GO:0006112; P:energy reserve metabolism; TAS.
 DR GO; GO:0007188; P:G-protein signaling, coupled to cAMP nucleo. .; TAS.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GFCRRHODOPS.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 Multigene family; Phosphorylation; Lipoprotein; Palmitate;
 Polymorphism; Diabetes mellitus; Obesity.
 KW DOMAIN 1 36 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 37 63 1 (POTENTIAL).
 FT DOMAIN 64 72 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT DOMAIN 92 111 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 112 133 3 (POTENTIAL).
 FT DOMAIN 134 155 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 156 178 4 (POTENTIAL).
 FT DOMAIN 179 203 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 204 225 5 (POTENTIAL).
 FT DOMAIN 226 292 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 293 314 6 (POTENTIAL).
 FT DOMAIN 315 326 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 327 347 7 (POTENTIAL).
 FT DOMAIN 348 408 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 8 8 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 26 26 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT DISULFID 110 189 BY SIMILARITY.
 FT LIPID 361 361 S-palmitoyl cysteine (By similarity).
 FT VARIANT 64 64 W -> R (in dbSNP:4994).
 FT VARIANT 265 265 T -> M (in dbSNP:4995).
 FT VARIANT 265 265 /FTid=VAR_003456.
 FT SEQUENCE 408 AA; 43519 MW; E98BD6C130DD977B CRC64;
 /FTid=VAR_014166.
 Query Match 12.4%; Score 230.5; DB 1; Length 408;
 Best Local Similarity 24.9%; Pred. No. 3.7e-10;
 Matches 93; Conservative 61; Mismatches 154; Indels 65; Gaps 14;
 QY 3 PGEALLAGLLVMVLAVALLS---NALVLCCVSAELRTRAGVLLNLSLGHLLAAL 58
 DB 34 PWEALAGAL---LALAVLATVGNLLVIVAIWTPRLQT-MTNVFTSLAAADLVWGLL 89
 QY 59 DMPFTLLGVNRGTPSAPGACQVIGFLDTFLASNAALSVAALSADOWLAVGFLPLRYAGRL 118
 DB 90 WPPAATLALTGHWPLGATGCLWTSVDVLCVTASITLICALAVDRYLAVTNPLRYGALV 149
 QY 119 RPRYAGLLLCANGQSALFSGALGCSW--LGYSAPASCSLRLPPEPEPPEPFAATATL 176
 DB 150 TKRCARTAVVLVWVSAVSAFAPMSQMWKVGADAEARQCH-----SNPRCCAFASNM 202
 QY 177 -----HAGVFLPLAVLCITSLQVHRVARRHC-----QRMDTVTKALA--- 215
 DB 203 PYVLSSVSFYLPLLVMLFVYARFVATRLRLRGELGRFPPEEPAPPSRLAPAP 262
 QY 216 ----LADLHPSVRQCLIOQKRHRATKIGIATATLFCAPYMTL-----AEL 265
 DB 263 VGTCAPEGPEVACGRPARLLPLREHRLCTGLINGTFTLCWLFPFLANVALGQPSL 322
 QY 266 VP---FVTVAQMGILSKLITYSKAVADPTYSL---LRPPFQVLGVMVHRLKKTTPRP 319
 DB 323 VFGPAFLAN--W-----LGYSAPFNPLIYCSDFRSAPFRLRCRRRL---PPEP 371
 QY 320 ASTHDSLSLVAGM 332
 DB 372 CAARPALFPGV 384
 RESULT 13
 B3AR MACMU
 ID B3AR MACMU
 AC Q28524;

PRT; 418 AA.

STANDARD;

Matches	95;	Conservative	56;	Mismatches	149;	Indels	67;	Gaps	15
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QY	3	PGEALLAGLVWVLAVALLS-----NALVLLCCAYSAELRTASGVTLVNLSLGHLLAAL	58
Db	34	PWAAALAGAL---LALAVLATVGGNLLVTAITRPLQT-MTNVFTVLSAAADLVWGLL	89
QY	59	DMPFTLLGVNMRGTPSAPGACOVIGFPLDTFLASNAALSVAALSADQMLAVGFPLRYAGRL	118
Db	90	VVPPAATLVLTGHWPLGATGCELWTSVDVLCVTASIEITLCALAVDRVLAVTNPLRYGALV	149
QY	119	RPRVAGLLCCANGQSIALPSGALGCSW--LGYSSAFASCISLUPPEPRPFAAFTATL	176
Db	150	TKRRARAANVVLVWVGAASFPATPISQWWRVGADBAORCH-----SNRCCAFASNM	202
QY	177	-----HAGVGVLPPLAVLCITLSQVHRVARRHCQMD-----TVMKALALLADLHPSV	224
Db	203	PYVLLSSSVSYFLPLLVMFLVYARVFWVATRQLRLRWELGRFPPESSPALSRSLAPAP	262
QY	225	RQRCGLIQ-----KRRHRATRKIGIAIATFLICFCFAPYVWTRL-----AEL	265
Db	263	AGTCAPPEGVPCACRRPARLLPLREHRACTUGLIMGITFTICWLPFFLVANVLRALGSPSL	322
QY	266	VP---FVTVAQMGILSKLCITYSKAVADPFTYSL---LRRPFRQVLAMVHRLKRTP--	317
Db	323	VPDPAFLALN--W-----LGVANSAPFNPLYICRSPDFRSAPFRLLCHCGGR-LPREPCA	373
QY	318	--REAST 322	
Db	374	ADRFASP 380	

RESULT 14			
ID	OX1R HUMAN	STANDARD;	PRT; 425 AA.
AC	O43613.		
DT	30-MAY-2000 (Rel. 39, Created)		
DT	30-MAY-2000 (Rel. 39, Last sequence update)		
DT	28-FEB-2003 (Rel. 41, Last annotation update)		
DE	Orexin receptor type 1 (Ox1r) (Hypocretin receptor type 1).		
GN	HCRT1R.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini, Hominidae; Homo.		
OX	NCBI_TaxId=9606;		
RN	[1]		
RN	SEQUENCE FROM N.A.		
RX	MEDLINE=98150861; PubMed=9491897;		
RA	Sakurai T., Amemiya A., Ishii M., Matsuzaki I., Chemelli R.M.,		
RA	Tanaka H., Williams S.C., Richardson J.A., Kozlowski G.P., Wilson S.,		
RA	Arch J.R.S., Buckingham R.E., Haynes A.C., Carr S.A., Annan R.S.,		
RA	McNulty D.E., Liu W.-S., Terrett J.A., Elshourbagy N.A., Bergsma D.J.,		
RA	Yanagisawa M.		
RT	"Orexins and orexin receptors: a family of hypothalamic neuropeptides		
RT	and G protein-coupled receptors that regulate feeding behavior."		
RL	Cell 92:573-585(1998).		
RN	[2]		
RN	REVIEW.		
RA	MEDLINE=21237974; PubMed=11340621;		
RA	Hungs M., Mignot E.		
RT	"Hypocretin/orexin, sleep and narcolepsy."		
RL	Bioessays 23:397-408(2001).		
RN	[3]		
RN	REVIEW.		
RA	MEDLINE=21178476; PubMed=11283317;		
RA	Willie J.T., Chemelli R.M., Sinton C.M., Yanagisawa M.;		
RT	"To eat or to sleep? Orexin in the regulation of feeding and		
RT	wakefulness."		
RL	Annu. Rev. Neurosci. 24:429-458(2001).		
CC	-I- FUNCTION: Moderately selective excitatory receptor for orexin-A		
CC	and, with a lower affinity, for orexin-B neuropeptide. Seems to be		
CC	exclusively coupled to the G(q) subclass of heteromeric G		
CC	proteins, which activates the phospholipase C mediated signaling		
CC	cascade (By similarity).		

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -----
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 CC -----
 CC EMBL; AF041243; AAC39601.1; -.
 CC Genew; HGNC:4848; HCRTR1.
 CC MIM; 602392; -.
 CC GO; GO:0005887; C: integral to plasma membrane; TAS.
 CC GO; GO:0004930; F: G-protein coupled receptor activity; TAS.
 CC GO; GO:0007631; P: feeding behavior; TAS.
 CC GO; GO:0007218; P: neuropeptide signaling pathway; TAS.
 CC GO; GO:0007268; P: synaptic transmission; TAS.
 CC InterPro; IPR000276; GPCR_Rhodopsn.
 CC InterPro; IPR004059; Orexin_receptor1.
 CC Pfam; PF00001; 7tm_1; 1.
 CC PRINTS; PR00237; GPCRHHODOPSN.
 CC PRINTS; PR01521; OREXINR.
 CC PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
 CC PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
 CC G-protein coupled receptor; Transmembrane.
 CC DOMAIN 1 46
 CC TRANSMEM 47 67
 CC DOMAIN 68 80
 CC TRANSMEM 81 102
 CC DOMAIN 103 119
 CC TRANSMEM 120 142
 CC DOMAIN 143 164
 CC TRANSMEM 165 185
 CC DOMAIN 186 216
 CC TRANSMEM 217 239
 CC DOMAIN 240 298
 CC TRANSMEM 299 321
 CC DOMAIN 322 336
 CC TRANSMEM 337 360
 CC DOMAIN 361 425
 CC CARBOHYD 194 194
 CC SEQUENCE 425 AA; 47521 MW; 1634083DE10CA092 CRC64;
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 CC Query Match 12.4%; Score 229.5; DB 1; Length 425;
 CC Best Local Similarity 25.3%; Pred. No. 4.5e-10;
 CC Matches 94; Conservative 55; Mismatches 154; Indels 69; Gaps 13;
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 CC 5 EALLAGLVNVALISNALVLLCCAYSAELRTRASGVLLNLSGLHLLAALDMPFTL 64
 CC 46 EWLLIARYAVFVVALVGNLTCLAVRNHMT-VTNYFVNLADVLVTAICLPASL 104
 CC 65 LGVNRGTPSAPGACQVIGFDLTFNLASNAALSAVALSADQWLVAGFPLRYAGRLRPYAG 124
 CC 105 LVDITESWLFQHALCKVPIYQVSVSVAVLTLSFIALDRWYAIChPLLFKSTAR-RARG 163
 CC 125 LLLGCWAGQSLAFSGAALGCSWLGYSAPASCSLRLLPPEPRFAA-----FTA 174
 CC 164 SILG-IWAVSLAI-----WVQAAYMECSVLPPELANRFLSVCDERWADLYPK 213
 CC 175 TLHVGFLP-LAVLCITSQVHRVARRHQRMDVTVMKALA-----LIADL----- 220
 CC 214 IYHSCFFIVTAPLGLMAYQIFRKLWGRQIPGTTGALVNRKRPSPDGLDLEQGLS 273
 CC 221 -HPSVORCL---IQQRREHRTKIGIAIAFLICEAP-----YVWTRLA--- 263
 CC 274 GEFPQGRFLAEVKQARRKAKMLMVLLVFLCYLPISVNLVLRVFGMFRQASR 333
 CC 264 ELVPFVTVAQWGLSKCLTYSKAVADPFTYSLLRPFQVL-----AGMVRHL 313
 CC 334 EAVYACFPESHW-----LVYNSAANPIYNFLSKGFKFQKAFSCCLPGLGPGCSLK 387

QY 314 KRTPRPASTHDS 325
 Db 388 APSFRSSASHKS 399
 RESULT 15
 SRS5_MOUSE
 ID SRS5_MOUSE STANDARD; PRT; 362 AA.
 AC O08858; O08998;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Somatostatin receptor type 5 (SSSR).
 GN SSTR5 OR SMSTR5.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SVJ; TISSUE=Liver;
 RX MEDLINE=97444289; PubMed=9300821;
 RA Lublin A.L., Diehl N.L., Hochgeschwender U.;
 RT "Isolation and characterization of the gene encoding the type 5 mouse
 RL (Mus musculus) somatostatin receptor (msst5).";
 RL Gene 195:63-66(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SVJ;
 RA Moldovan S., Demayo F., Brunicardi F.C.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Liver;
 RA Gordon D.F., Woodmansee W.W., Wood W.M., Knauf H., James R.A.;
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SVJ;
 RA Baumeister H., Roosterman D., Schafer J., Kreuzer O., Meyerhof W.;
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Receptor for somatostatin-28. The activity of this
 CC receptor is mediated by G proteins which inhibit adenylyl cyclase.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC -----
 CC EMBL; U02697; AAC53353.1; -.
 CC EMBL; AF004740; AAB61418.1; -.
 CC EMBL; AF030441; AAB86492.1; -.
 CC EMBL; AF035777; AAB88302.1; ALT_INIT.
 CC HSP; P02699; 1P88.
 CC MGD; MGI:894282; Sstr5.
 CC InterPro; IPR000276; GPCR_Rhodopsn.
 CC Pfam; PF00001; 7tm_1; 1.
 CC PRINTS; PR00237; GPCRHHODOPSN.
 CC PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
 CC PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein;
 CC Multigene family; Lipoprotein; Palmitate.
 CC DOMAIN 1 35
 CC TRANSMEM 36 63
 CC DOMAIN 64 73
 CC TRANSMEM 74 99
 CC DOMAIN 100 110
 CC TRANSMEM 111 132
 CC DOMAIN 111 132
 CC TRANSMEM 111 132

FT	DOMAIN	133	154	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	155	175	4 (POTENTIAL).
FT	DOMAIN	176	195	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	196	220	5 (POTENTIAL).
FT	DOMAIN	221	246	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	247	272	6 (POTENTIAL).
FT	DOMAIN	273	282	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	283	307	7 (POTENTIAL).
FT	DOMAIN	308	362	CYTOPLASMIC (POTENTIAL).
FT	CARBOHYD	13	13	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	23	23	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	185	185	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DISULFID	109	184	BY SIMILARITY.
FT	CONFLICT	99	99	V -> VV (IN REF. 1).
FT	CONFLICT	303	305	YGF -> LWL (IN REF. 2).
SQ	SEQUENCE	362 AA;	39948 MW;	AA091DDDS70DFAB CRC64;
Query Match 12.3%; Score 229; DB 1; Length 362;				
Best Local Similarity 25.7%; Pred. No. 4.2e-10;				
Matches 95; Conservative 53; Mismatches 162; Indels 60; Gaps 13;				
QY		1	MGPGGALLAGLLVMVLAVALLSNALVLLCCAYSAELRTRASGVLLVNLGLHLLAALDM	60
Db		33	MGARAVLPVLYLLVCTVGLGNTLVIYVLRVYAKMT-VTNVYILNLAADVLF-MLGL	90
QY		61	PPTLLGVNRGRTSPAGACQVIGLDTFTLASNALSVAAALSADQWLA VGFPLRYAGRLRP	120
Db		91	PFLATQNAVSYWFFGSLCRLVMTLDGINQFTSIFCLMVMSVDRLAVVHPLRSARWRP	150
QY		121	RYAGLLGCAGQSLAFSGAALGCSWLGYSAGFASCSLRLPPEPERPFAAFTATLHVG	180
Db		151	RVAKLASAAVWVPSLLMSPLL--VPADVQEGWGTCNLSW-PEPVGLWGAAFIYTSVLG	207
QY		181	FVLPLAVLCLTSLQVHRVARHRCQRMQVTWKALALADLHPSVQRCLIOCKRRHRAT	240
Db		208	FRGPLLVICL-----CYLLIVVKVKAAGRVG---SSRRR-----ESERKVT	246
QY		241	RKIGIAIATFLICFAPYVWTRLAEL--VPFVTVNAQWGLSKCLTYSKAVADPPTYSL	297
Db		247	RMVVVVVLVFGCWLPPFFIVNVLNLAFTLPEPTSGAGLYFFVWVLSYANSCANLLYGFL	306
QY		298	----RPFRQVLAGMVHRLK-----TPRPASTHDSLSLDVAGMVHQLKRTFRP	343
Db		307	SNFRQSFKALC-----LRGYGVEDADAEPRP-----DKSGRPQTTL---PTR	349
QY		344	ASTHNGSVDT	353
Db		350	SCEANGLMQT	359

Search completed: May 18, 2004, 12:07:09
Job time : 20 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 18, 2004, 12:03:02 ; Search time 46 Seconds
(without alignments)
2489.850 Million cell updates/sec

Title: US-10-049-569-2

Perfect score: 1858

Sequence: 1 MGPGELLAGLLVMYLAVAL.....ASTHNGSVDTENDSCLOQTH 363

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	250.5	13.5	438	11 Q63004	Q63004 rattus norv
2	246.5	13.3	390	13 Q8QGQ4	Q8QGQ4 carassius a
3	238.5	12.8	380	13 Q8DGG6	Q8DGG6 carassius a
4	237	12.8	370	13 Q8UML5	Q8UML5 fugu rubrip
5	237	12.8	399	5 Q8GME4	Q8GME4 caenorhabdi
6	237	12.8	402	5 Q8GME5	Q8GME5 caenorhabdi
7	233	12.5	478	11 Q8BLD9	Q8BLD9 mus musculu
8	231.5	12.5	353	13 Q9YHY3	Q9YHY3 lampetra fl
9	230.5	12.4	425	4 Q9HBV6	Q9HBV6 homo sapien
10	230	12.4	367	6 Q8MI04	Q8MI04 ovis aries
11	229.5	12.4	340	13 Q9YHY2	Q9YHY2 lampetra fl
12	229	12.3	385	11 Q9TK40	Q9TK40 mus musculu
13	228.5	12.3	437	13 Q42316	Q42316 cyprinus ca
14	227.5	12.2	367	13 Q9PVG0	Q9PVG0 carassius a
15	227.5	12.2	391	5 Q96716	Q96716 branchiosto
16	227.5	12.2	477	4 Q8NEQ8	Q8NEQ8 homo sapien

17	227	12.2	380	13 Q42317	Q42317 cyprinus ca
18	226.5	12.2	358	11 Q9QX37	Q9QX37 mus musculu
19	226.5	12.2	397	11 Q9D282	Q9D282 mus musculu
20	226	12.2	390	13 Q8AXM7	Q8AXM7 carassius a
21	224	12.1	367	13 Q9PVF9	Q9PVF9 carassius a
22	223.5	12.0	371	11 Q8BK80	Q8BK80 mus musculu
23	223	12.0	387	4 Q96K10	Q96K10 homo sapien
24	222.5	12.0	385	11 Q8BQ97	Q8BQ97 mus musculu
25	222.5	12.0	447	6 Q8SPH2	Q8SPH2 sus scrofa
26	222	11.9	388	4 Q8LXH9	Q8LXH9 homo sapien
27	221.5	11.9	446	13 Q42315	Q42315 cyprinus ca
28	221	11.9	445	13 Q98841	Q98841 anguilla an
29	220.5	11.9	388	5 Q8MTW6	Q8MTW6 spisula sol
30	220	11.8	397	4 Q725R9	Q725R9 homo sapien
31	219.5	11.8	215	6 Q9GKP7	Q9GKP7 sus scrofa
32	219	11.8	470	11 P37842	P37842 rattus norv
33	218	11.7	394	5 Q9NHF3	Q9NHF3 alypsia cal
34	217	11.7	452	13 Q7T2S8	Q7T2S8 carassius a
35	216.5	11.7	346	6 Q95XS6	Q95XS6 ovis aries
36	216	11.6	460	5 Q8GME6	Q8GME6 caenorhabdi
37	215	11.6	331	13 Q801F3	Q801F3 fugu rubrip
38	214	11.5	385	4 Q86VF2	Q86VF2 homo sapien
39	214	11.5	559	11 Q9QW71	Q9QW71 rattus sp.
40	213.5	11.5	518	6 Q9MRT8	Q9MRT8 cryptolagus
41	212	11.4	394	5 Q9NJS6	Q9NJS6 alypsia kur
42	211.5	11.4	352	13 Q9YHY4	Q9YHY4 lampetra fl
43	211	11.4	445	13 Q98842	Q98842 anguilla an
44	210.5	11.3	459	11 Q8CGI5	Q8CGI5 mus musculu
45	210.5	11.3	515	11 Q9DBL0	Q9DBL0 mus musculu

ALIGNMENTS

RESULT 1

Q63004 PRELIMINARY; PRT; 438 AA.
ID Q63004
AC Q63004;
DT 01-NOV-1996 (TREMREL. 01, Created)
DT 01-NOV-1996 (TREMREL. 01, Last sequence update)
DE 01-OCT-2003 (TREMREL. 25, Last annotation update)
DE 5-HT6 serotonin receptor.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Striatum;
RX MEDLINE=96102917; PubMed=8522988;
RA Kohen R., Metcalf M.A., Khan N., Druck T., Huebner K., Lachowicz J.E.,
RA Meltzer H.Y., Sibley D.R., Roth B.D., Hamblin M.W.;
RT "Cloning, characterization, and chromosomal localization of a human 5-
RT HT6 serotonin receptor."
RL J. Neurochem. 66:47-56(1996).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; L41146; AAA92633.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0001861; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm1; 1.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR; 1.
DR PROSITE; PS00262; G-PROTEIN RECEPTOR; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 438 AA; 46786 MW; DB90403892P691A9 CRC64;

Query Match 13.5%; Score 250.5; DB 11; Length 438;
Best Local Similarity 24.7%; Pred. NO. 7e-13;
Matches 98; Conservative 69; Mismatches 176; Indels 53; Gaps 14;

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QY 2 GPGEA-----LLAGLLVMVLAVALLSNALVLLCCAYSAELRTRASGVLLVNLISLGH 53
DB 16 GPGEPPAPGGGWAAALCVVILVTAANSLVILCTQPAVRNT--SNFFLVSLFTSD 73
QY 54 LLAALDMPFTLLGMGRGTSAPGACOVIGFLDTFLASNAALSVAAALSADQWLVAGPPLRYAGRLRYAGLL 113
DB 74 MVGLVMPANALYGRWVLARGLCLWTFADVMCCSAILNCLISIDRYLLILSPUR 133
QY 114 YAGRL-RPRYAGLLGCWAGQSLA----FSGAALGCSWLGYSYSAFASCSLRLPPEPR 168
DB 134 YKLRMTAPRALALILG-AW--SLAALASFLPPLLGHGELKART-----PAPGQCR 181
QY 169 FAA---FTAILHAGFVLPLAVLCILTSLOWHRVARRHCQMDVT-----MKALALLA 218
DB 182 LLASLPVLVAGVTFPLPSGACFTYCRILLARQAQVVASLTGTGAQALLETLOVPR 241
QY 219 DLHPSVR---QRCLIOQKRHRATRKIGIAIATFLICFAPYVMTRLAELVFPFVNAQ 274
DB 242 TPREGMESADSRRLATKSHRKALKASITGLILGMFPVTLWPFVFNIAQAQVDCISPG 301
QY 275 WGLSKCLTYSKAVADPFTYSLRRPPROVLGAW-----HRLKTPRPASTHDS 326
DB 302 FDVLT-WLGYCNSTMPILYPLFMRDPRALGRFLPCVHCOPPEHRASPSPSWTSHSGA 360
QY 327 LDVAGMVHOLLKRTPRPASTHNGSVDTENDSCILQOT 362
DB 361 R--BGLSQVLPPLPFPNSDSGA-SGTSGLQLT 393

RESULT 2
Q80GQ4 PRELIMINARY; PRT; 390 AA.
ID Q80GQ4
AC Q80GQ4;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Type five-like somatostatin receptor.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OC NCBI_TaxID=7957;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=20453044; PubMed=10996426;
RA Lin X., Janovick J.A., Cardenas R., Conn P.M., Peter R.E.;
RT "Cloning and expression of a type five-like somatostatin receptor in
RT goldfish."
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AF252879; AAM18805.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . . IEA.
DR InterPro; IPR001092; HLH_Basic.
DR InterPro; IPR001092; HLH_Basic.
DR Pfam; PF00001; 7tm1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G-PROTEIN RECP F1_1; 1.
DR PROSITE; PS00262; G-PROTEIN RECP F1_2; 1.
DR G-protein coupled receptor; Receptor; Transmembrane.
DR InterPro; IPR001092; HLH_Basic.
DR G-protein coupled receptor; Receptor; Transmembrane.
KW SEQUENCE 390 AA; 44136 MW; EC1219A4B6CF9A8 CRC64;

Query Match 13.3%; Score 246.5; DB 13; Length 390;
Best Local Similarity 23.9%; Pred. No. 1.3e-12;
Matches 79; Conservative 59; Mismatches 122; Indels 71; Gaps 10;

QY 7 LLAGLLVMVLAVALLSNALVLLCCAYSAELRTRASGVLLVNLISLGHLLAALDMPFTLLG 66
DB 42 ILAVIYLVVVGLTGNSLAIFVVLRYTKMT-ATNMYILNLAVADELY-ILGLPFLTAH 99

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QY 67 VMGRGTSAPGACOVIGFLDTFLASNAALSVAAALSADQWLVAGPPLRYAGRLRYAGLL 126
DB 100 NMLGYWPFNGFLCRLMTWTSISOFTSTFCLTVMSIDRYMAVWHPISARWRRPRVAKVI 159
QY 127 LGCAWGQSLAFSGAALGCSWLGYSYSAFASCSLRP-----PEPERPR 168
DB 160 NSMVA-----LSCLLTPLVILYCDVQPELNTCNLSWPEPRDVW 198
QY 169 FAATATLHAGFVLPLAVLCILTSLOWHRVARRHCQMDVTMKALALLADLHSHVQRQC 228
DB 199 STAFILYAMLGFFFLMVICL-----CYLLIVIKVKSASARAGLS----- 239
QY 229 LIQOKRHRATRKIGIAIATFLICFAPYVMTRLAELVFPFVNA-OWGI--LSKCLTYS 285
DB 240 --KGRSEKKVTRMVVIVVFLVCLWPPFIINILNLSITLPENSLMTGIVFLVILTYV 297
QY 286 KAVADPFTYSL-----RPPRQVLAGMVHRL 312
DB 298 NSCANPLLYSLSDNFKRSFOQLC--IHKV 326

RESULT 3
Q8DQG6 PRELIMINARY; PRT; 380 AA.
ID Q8DQG6
AC Q8DQG6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Somatostatin receptor type two.
DE SST2.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OC NCBI_TaxID=7957;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=20453044; PubMed=10996426;
RA Lin X., Janovick J.A., Cardenas R., Conn P.M., Peter R.E.;
RT "Molecular cloning and expression of a type-two somatostatin receptor
RT in goldfish brain and pituitary."
RL Mol. Cell. Endocrinol. 166:75-87(2000).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AF139597; AAF98367.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . . IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G-PROTEIN RECP F1_1; 1.
DR PROSITE; PS00262; G-PROTEIN RECP F1_2; 1.
DR G-protein coupled receptor; Receptor; Transmembrane.
DR InterPro; IPR001092; HLH_Basic.
DR G-protein coupled receptor; Receptor; Transmembrane.
KW SEQUENCE 380 AA; 43146 MW; CE897F7537CFA30 CRC64;

Query Match 12.8%; Score 238.5; DB 13; Length 380;
Best Local Similarity 24.1%; Pred. No. 6.1e-12;
Matches 84; Conservative 63; Mismatches 163; Indels 39; Gaps 9;

QY 14 MYLAVALLSNALVLLCCAYSAELRTRASGVLLVNLISLGHLLAALDMPFTLLGVNRGRT 73
DB 60 VYVAVGLCGNALVMVILRYAKMT-VTVIYILNLAVAD-VLCMLSLFFIALQLSLHWP 117
QY 74 SAPGACOVIGFLDTFLASNAALSVAAALSADQWLVAGPPLRYAGRLRYAGLLGCAGQ 133
DB 118 FGSACRVVLTADSMNQFTSIFFLVMSFDRLAVVHPDKTKWKPKRMAKSISLAMVVI 177
QY 134 SLAFSGAALGCSWLGYSYSAFASCSLRLPPEPRFAAFTATLHAGFVLPLAVLCILTS 193
DB 178 SLVNLPIIMYSGVNVKKNKNEARTCNLWPEPQNTYITVFYFFFMGFLPLVICM--- 234

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QY 194 QVHRVARRHQRMDVTVMKALLADLHPSVQRCLIQKRRHRATRKIGIAIATFLIC 253
Db 235 -----CYLLIVIKVS-----SGRVSSKSKRKSRKVTWMSIVVVVFLC 276
QY 254 FAPYV---MTRLAELVPFVTVNAQWILSKCLITYSKAVADPTYSLL-----RRPRQVLA 306
Db 277 WLPFYFVNTSVTGTPTTVPVLKSTDFVVLVGYANSCANFIFYAFSLDNFKKSFQNVLC 336
QY 307 GMVHRLKTRP--RPASTHSDSLDVAGMVHOLLKTRTPRPASTHNGSVDT 353
Db 337 -----LKRUGGLDEIERSDQRDRMVDVMSSET-HNAALLNGDLQT 378

RESULT 4
Q8UWL5 PRELIMINARY; PRT; 370 AA.
AC Q8UWL5, 201-JUN-2003 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Somatostatin receptor 2.
GN SSTR2.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OC NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21564205; PubMed=11707075;
RA Bagheri-Fam S., Ferraz C., Demalle J., Scherer G., Pfeifer D.;
RT "Comparative Genomics of the SOX9 Region in Human and Fugu rubripes:
RT Conservation of Short Regulatory Sequence Elements within Large
RT Intergenic Regions.";
RL Genomics 78:73-82(2001).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AF329945; AAU32173.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G-PROTEIN RECEPT_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN RECEPT_F1_2; 1.
DR G-protein coupled receptor; Receptor; Transmembrane.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 370 AA; 41364 MW; 420BB12F204946B6 CRC64;

Query Match 12.8%; Score 237; DB 13; Length 370;
Best Local Similarity 22.9%; Pred. No. 7.9e-12;
Matches 86; Conservative 61; Mismatches 133; Indels 96; Gaps 14;

QY 14 MVLAVALLSNALLCCAYSAELTRASGVLLVNLISGLHLLAALDMPFTLLGVMRGTRP 73
Db 53 LVCAVGLGCLNALVIYILRYAKMKT-VTHYIILNLAADVLP-MLGLPIAQLALVHP 110
QY 74 SAGACQVIGFLDTFLASNAALSAVALSADQWLVGFLPRYAGRLRPVYAGLLGCGAQ 133
Db 111 FGPVLGRVMTVDLSNQFTSIFCLAVMSIDRYLAVVHPKSTKWRKPRVAKTINVAVMA 170
QY 134 SLA-----FSGAAL--GCSWLGYSSAFASCLRLPPEPRPFAATLHAGVFL 183
Db 171 SLVNVLPVIYSIIITKQDC-----FCTI-VWPEPEAYTAFMYTFLIGFL 219
QY 184 PLAVLCITSLQVHRVARRHCQRMDVTVMKALLADLHPSVQRCLIQKRRHRATRKI 243
Db 220 PLLVISL-----CYVPIIVKVKSSGIRVGSS-----KKRGRKVRTRV 258
QY 244 GIAIAFLICFAPYVMTLAEV-----PFYTVNAQWILSKCLITYSKAVAD 290

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Db 259 SIIVAVFVLCWLPFYFVNTSVTGSISATHVLRSTFAFVV-----LGVANSCAN 308
QY 291 PFTYSLRLRRPR-----QVLGVMVHLLKRTPRPASTHSDSLDVAGMVHOLLKTRP 341
Db 309 PILYAFISENFKSKFQNVLCGLQKVGGL-----DEAERSDQRQKSRMIND----- 353
QY 342 RPASTH-----NGSVDT 353
Db 354 -PTETSTRLLNGDLQT 368

RESULT 5
Q86ME4 PRELIMINARY; PRT; 399 AA.
AC Q86ME4;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Hypothetical protein F15A8.5.
GN F15A8.5.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OC NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA Waterston R.;
RA "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=Bristol N2;
RA Miller N.;
RT "The sequence of C. elegans cosmid F15A8.";
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; U97549; AA091738.1; -.
DR WormPep; F15A8.5c; CE33617.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti. .; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR000412; ABC_transport2.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G-PROTEIN RECEPT_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN RECEPT_F1_2; 1.
DR Hypothetical protein.
KW Hypothetical protein.
SQ SEQUENCE 399 AA; 45526 MW; 40629EF6E074D048 CRC64;

Query Match 12.8%; Score 237; DB 5; Length 399;
Best Local Similarity 23.2%; Pred. No. 8.6e-12;
Matches 82; Conservative 61; Mismatches 142; Indels 68; Gaps 11;

QY 8 LAGLLVAVLVALSNALLCCAYSAELTRASGVLLVNLISGLHLLAALDMPFTLLGV 67
Db 8 LLGFLSVLITLAFGNLLVCAAILNDLSLRKQENFLVSLAVSDLLVSVLWMLFAVND 67
QY 68 MRGTPSAGACQVIGFLDTFLASNAALSAVALSADQWLVGFP---LRYAGRLRPYAG 124
Db 68 ILGWPFQGFQVFCQFWISFDITCTTASILNLCALSLDRYWHISRPVYIRYCNRRINVI 127

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Qy	125	LLLCGAWGSLAFSGAALGCSWLGYS	-----AFASCSRLPLPPPERPRFAATATL 178
Db	128	VLV--WLSAGIGAAPLG--	-----FGFGSKVTNNITGLPVCEMRLP-----LPYAIGS 173
Qy	177	HAVGFVLPLAVLCLTSLQVHRVARRHCCORMDTVMKALLL	-----ADLHPSVROR 227
Db	174	SNVSFPLPAWVVIITKLYLYARKHVSIKTOLQQATSLMLQASEKIREITSIFS 233	
Qy	228	-----CLIQOKRR	-----HRAIRKIGIAATATFLICAPYVWTR----- 261
Db	234	LNFLCPTREFKNQSPQDEHTPAAHNRSNISQKARLTGLVIMGTFLVCMWLPFTVNILRA 293	
Qy	262	-LAEILVPFVTVA--QWILSKCLTYSKAVADPFTYSLLRPPFROVLAMVHRL 312	
Db	294	WLPEFSSKTIWVTV-----LGYANSSANPLIYSIFNRDFRAFKKIIVRV 340	
RESULT 6			
Q86MES		PRELIMINARY;	PRT; 402 AA.
ID	Q86MES		
AC	Q86MES		
DT	01-JUN-2003	(TREMBLrel. 24, Created)	
DT	01-JUN-2003	(TREMBLrel. 24, Last sequence update)	
DT	01-OCT-2003	(TREMBLrel. 25, Last annotation update)	
DE	Hypothetical protein F15A8.5.		
GN	F15A8.5.		
OS	Caenorhabditis elegans.		
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;		
OC	Rhabditidae; Pelodierinae; Caenorhabditis.		
NCBI_TaxID	6239;		
LN	[1]		
RC	SEQUENCE FROM N.A.		
RP	STRAIN=Bristol N2;		
RC	MEDLINE=99069613; PubMed=9851916;		
RX	Waterston R.;		
RA	"Genome sequence of the nematode C. elegans: a platform for		
RT	investigating biology. The C. elegans Sequencing Consortium."		
RL	Science 282:2012-2018(1998).		
RL	[2]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=Bristol N2;		
RA	Miller N.;		
RT	"The sequence of C. elegans cosmid F15A8.,"		
RL	Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.		
RL	[3]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=Bristol N2;		
RA	Waterston R.;		
RL	Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.		
RL	EMBL; U97549; AAC91737.1; -		
DR	WormPep; F15A8.5b; CE33616.		
DR	GO; GO:0016021; C:integral to membrane; IEA.		
DR	GO; GO:0005524; F:ATP binding; IEA.		
DR	GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti. . . ; IEA.		
DR	GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.		
DR	GO; GO:0007186; P:G-protein coupled receptor protein signalin. . . ; IEA.		
DR	GO; GO:0006810; P:transport; IEA.		
DR	InterPro; IPR000412; ABC transp2.		
DR	InterPro; IPR000276; GPCR_Rhodpsn.		
DR	Pfam; PF00001; 7tm 1; 1.		
DR	PRINTS; PR00237; GPCRHDOPSN.		
DR	PROSITE; PS00890; ABC2_MEMBRANE; 1.		
DR	PROSITE; PS00237; G_PROTEIN_RECEP_Fl_1; 1.		
DR	PROSITE; PS00262; G_PROTEIN_RECEP_Fl_2; 1.		
KW	Hypothetical protein.		
SO	SEQUENCE 402 AA; 06ABE42C0970CBF5 CRC64;		

Query Match 12.8%; Score 237; DB 5; Length 402;
Best Local Similarity 23.2%; Pred. No. 8.7e-12;
Matches 82; Conservative 61; Mismatches 142; Indels 68; Gaps 11;
Qv 8 IAGHIVMVAIVALLSNALVLLCCRYSAETRTASGVLLVNI SLGHLLLAALDMPTFLGV 67

[illegible]

	Query Match	12.5%;	Score 233,	DB 11:	Length 478;
	Best Local Similarity	22.9%;	Pred. No. 2.3e-11;		
	Matches 82; Conservative	76;	Mismatches 146;	Indels 54;	Gaps 13;
Qy	1	MGPEALLAGLLVWVLAVALLSNALVILLCCAYSAEELRTASGVLLVNLSLGHLLLAALDM	60		
		::::: ::::			
Dd	34	LGPAAVVVTAGLLTLIIWTLLGNLVLCATIVRSRHRLAKMTNIFIVSLAUSDLFVALLVM	93		
		::: :::: ::::			
Qy	61	PFYLLGWGRGRTSARGA-CQVGFDLTPLASNAAALSVAALSADOMLAVGFPPRYACGLR	119		
		: : : : : :			
Dd	94	PWKAVEAVGYWPFF--GAFCDIWAFEDIMCSTASILNLCTIISVDRIWAISRFPFRYEKMT	151		
		: : : : : :			
Qy	120	PRVAGLLLGCAWGQQSIASFSGAALGCSSN---LGYSSAFASCURLPPE-----	163		
		: : : : : :			

Db 152 QRVALVWALAWTLISLIFIPVQLNWRDKAGSQREGLLSNLTPWEEGWELDQRTENC 211
Qy 164 -PERPFAAFTATLHAGVFLPLAVLCLTSLOVHRVARRHCORMDVTVMKALLADLHP 222
Db 212 DSLNRYAISLSS--ISYIPVIMVITYRIYIAQVQIRR-----ISSLERAAHQ 264
Qy 223 SVQR-----CLIOQRRHRHATKIGIAIATFICFAPYVMTLAEVLVFTVNAQM 275
Db 265 SCRSRGACEPDPPLSRASIKETKVFRTLSVINGVFVCCWLPFFI--LNCMVFCSSGDAQ 322
Qy 276 GILS--KCLT-----YSKAVADPFTYSL--LRPFRVLGVMVHLLKRT 317
Db 323 GPRGFCVSETTFDFVWFGWANSNLPIIAFNADPRKVAQLL-GCSH-LCRTP 378

RESULT 8
Q9HYH3 PRELIMINARY; PRT; 353 AA.
AC Q9HYH3, 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DE Putative odorant receptor LOR4.
OS Lampetra fluviatilis (River lamprey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC Petromyzontiformes; Petromyzontidae; Lampetra.
OX NCBI_TaxID=7748;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Olfactory organ;
RA Berghard A., Dryer L.;
RT "A novel family of ancient vertebrate odorant receptors.";
RL J. Neurobiol. 0:0-0(1998).
CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AF069547; AAC82382.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR InterPro; IPR001092; HLH_Basic.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G PROTEIN RECEPTOR FL1; 1.
DR PROSITE; PS00262; G PROTEIN RECEPTOR FL2; 1.
DR PROSITE; PS00038; HLH 1; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 353 AA; 39901 MW; D89F8D6FC627180 CRC64;

Query Match 12.5%; Score 231.5; DB 13; Length 353;
Best Local Similarity 22.0%; Pred. No. 2.2e-11;
Matches 76; Conservative 88; Mismatches 147; Indels 35; Gaps 10;

Qy 1 MGPEALLAGLVWVAVALLSNALVLLCCAYSAELTRASGVLLVNLGLHLLAALDM 60
Db 28 MSRTAALSATITLILA-TVLGNLLIITSIAVFRQLQTR-TNIALSLAVADLLVGLVTM 85
Qy 61 PFTLLGWGRGTPSAPCAQVIGLDTFLASNAALSVAAALSADQMLAVGFPLRYAGRLRP 120
Db 86 PYSMMKAVYKCFYGOFFCNQLQVFLDYMLTNSIMHLGCIADRYVAICDPLRYQRTVN 145
Qy 121 RYAGLLGCGWAGSLAFSGAALCGSLWGYSSAFASCLRLPPEPRPFAATATHAVG 180
Db 146 HTVVTMLLSWFGPALFSSPIL-----VFNFPMSRGNIEIISCPNQCLFFVSTWLVSVVG 201
Qy 181 ---FVLPLAVLCLTSLOVHRVARRHCORMDVTVMKALLADLHPSVROR-----CLIQ 231
Db 202 VCPYVLSLTMSTVYARIIVARRQRISSVLSQ-----VHAQOQQOQQAFTNIR 254
Qy 232 QK-----RRHRAATKIGIAIATFICFAPYVMTLAEVLVFTVNAQMGLSKCLTYSKA 287
Db 255 QKWAMKREHSAKTLGSIIGVYLLSWLFPYVMVL--PFENFQNSAAVRITTWIGYISS 312

Qy 288 VADPFTYSLRRPPRQVLGAVH-RLIKRTPRPASTHDSLSLDVAGM 332
Db 313 AINPVLVATLNRPPSAFVAISKVL-----SSTRARTMDLSGV 352

RESULT 9

Q9HBV6 PRELIMINARY; PRT; 425 AA.
AC Q9HBV6, 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypocretin receptor-1.
GN HCRIR1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20429525; PubMed=10973318;
RA Peyron C., Faraco J., Rogers W., Ripley B., Overeem S., Charnay Y.,
RA Nevimalova S., Aldrich M., Reynolds D., Albin R., Li R., Hungs M.,
RA Pedrazzoli M., Padigar M., Kuchelapati M., Fan J., Maki R.,
RA Lammers G.J., Bouras C., Kuchelapati R., Nishino S., Mignot E.;
RT "A mutation in a case of early onset narcolepsy and a generalized
RT absence of hypocretin peptides in human narcoleptic brains.";
RL Nat. Med. 6:991-997(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Yeager M., Welch R., Haque K., Bergen A.;
RT "Genomic sequence of the hypocretin (orexin) receptor 1 (HCRTR1).";
RL Submitted (DSC-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21580342; PubMed=11723285;
RA Olafsdottir B.R., Rye D.B., Scammell T.E., Matheson J.K.,
RA Stefansson K., Gulcher J.R.;
RT "Polymorphisms in hypocretin/orexin pathway genes and narcolepsy.";
RL Neurology 57:1896-1899(2001).
DR EMBL; AF202084; AAG28020.1; -.
DR EMBL; AF202078; AAG28020.1; JOINED.
DR EMBL; AF202079; AAG28020.1; JOINED.
DR EMBL; AF202080; AAG28020.1; JOINED.
DR EMBL; AF202081; AAG28020.1; JOINED.
DR EMBL; AF202082; AAG28020.1; JOINED.
DR EMBL; AF202083; AAG28020.1; JOINED.
DR EMBL; AF202089; AAL50221.1; -.
DR EMBL; AY062030; AAL47214.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016499; F:orexin receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR InterPro; IPR004059; Orexin_receptor1.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PRINTS; PR01521; OREXIN1R.
DR PROSITE; PS00237; G PROTEIN RECEPTOR FL1; 1.
DR PROSITE; PS00262; G PROTEIN RECEPTOR FL2; 1.
KW Receptor.
SQ SEQUENCE 425 AA; 47535 MW; B650B37F3A2CA096 CRC64;

Query Match 12.4%; Score 230.5; DB 4; Length 425;
Best Local Similarity 25.3%; Pred. No. 3.3e-11;
Matches 94; Conservative 55; Mismatches 154; Indels 69; Gaps 13;

Qy 5 EALLAGLVWVAVALLSNALVLLCCAYSAELTRASGVLLVNLGLHLLAALDMPTFL 64
Db 46 EWLIIAYAVFVYVALVGNLTCLVAVRNHMRIT-VTNYFVNLSLADLVITACLPASL 104

QY 65 LGVNRGRTSPAGACQVIGFDTFLASNAALSVAALSDADQWLVAGFPLRYAGRLPRYAG 124
 Db 105 LVDITESWLFCHALCKVPIYQAVSVSVAVITLSFIALDRWYAICHPELLFKSTAR-RARG 163
 QY 125 LLLCANGOSLAFSGAALGCSWLGYSAPASCRLRPPERPRFAA-----FTA 174
 Db 164 SILG-IWAVSLAI-----WVQAAVMECSVLPELANRTRLPSCVDCRWDADLYPK 213
 QY 175 TLHVGFLP-LAVCLTSLQVHRVARRHCQMDVTVMKALA-----LLADL----- 220
 Db 214 IYHSCFFIVT-LAPGLMAYAFQIFRKLNGRQIPGTTLSALVRNWKRPSPQLGDLBQGLS 273
 QY 221 -HPSVRGCL---IQKRRHRATRKIGIALIFLCFAP-----YVTRLA--- 263
 Db 274 GEPQFRARAFLEVKOMRARKTKAKMLVMVLLNFPALCYLPISVLNVLKRVFGMFRQASDR 333
 QY 264 ELVPFVTNAQWGLSKCLTYSKAVADPFTYSLRRRFRQVL-----AGMVERHL 313
 Db 334 EAVYACTFESH-----LVYNSAANPIIYNFLSGKFRQFKAAPSCCLPG-LGPCSLK 387
 QY 314 KRTPRPASTHDS 325
 Db 388 APSPRSASHKS 399

RESULT 10

QMI04 QMI04 PRELIMINARY; PRT; 367 AA.
 AC QMI04;
 DT 01-OCT-2002 (TREMELrel. 22, Created)
 DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)
 DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
 DE Somatostatin receptor subtype 5.
 GN SS15.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pituitary;
 RA Debus N., Dutoir A., Boudouresque F., Vuaroqueaux V., Oliver C.,
 RA Ouafik L.;
 RT "Molecular cloning and tissue distribution of the ovine somatostatin
 receptor subtype 5: ossf5";
 RT Submitted (APR-2002) to the EMBL/GenBank/DBSJ databases.
 RL [2]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Pituitary;
 RA Debus N.;
 RT "Regulation of GH secretion in sheep: Role of somatostatin and its
 receptors";
 RL Thesis (1999).
 RL Department of Interdisciplinary communications in Endocrinology,
 RL University of Aix-Marseille II, Marseilles, France.
 DR EMBL; AJ441116; CAD9615.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin...; IEA.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm1; 1.
 DR PRINTS; PR00237; GPCRHHODOPSN.
 RL Department of Interdisciplinary communications in Endocrinology,
 RL University of Aix-Marseille II, Marseilles, France.
 DR EMBL; AJ441116; CAD9615.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin...; IEA.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm1; 1.
 DR PRINTS; PR00237; GPCRHHODOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 KW Receptor.
 FT CHAIN 2 367 SOMATOSTATIN RECEPTOR SUBTYPE 5.
 SQ SEQUENCE 367 AA; 40269 MW; FASCA87A8ABED764 CRC64;
 Query Match 12.4%; Score 230; DB 6; Length 367;
 Best Local Similarity 26.2%; Pred. No. 3.1e-11;
 Matches 79; Conservative 51; Mismatches 138; Indels 34; Gaps 8;

QY 11 LILVMVALLSNALVLLCCAYSALRTRASGVLLVNLSLGHLIALDMPFTLLGVNRG 70
 Db 46 LYLVCVAGLGGNALVIVVLRHAKMT-VTNVITLNAVADVLL-MLGLSFVATQNAIS 103
 QY 71 RTPSPAGACQVIGFDTFLASNAALSVAALSDADQWLVAGFPLRYAGRLPRYAG 130
 Db 104 YWPFGEVLCRLVMTLDGINQFTSIFCLTVMSVDRYLVAVVHPIRSRWRPRVAKLASAAV 163
 QY 131 WQSLAFSGAALGCSWLGYSAPASCRLRPPERPRFAAFTATLHAGVFLPLAVLCL 190
 Db 164 WAFSLVMSLPLV--VFADIQGMNTCNLTW-PEPVGLMGAVFIYTSVLGFFGLLVICL 220
 QY 191 TSLQVHRVARRHCQMDVTVMKALALLADLHPSVQRCLIQKRRHRATRKIGIAIATF 250
 Db 221 -----CYLVIVVVKLAKSGV-----RVGSTRRSERKVTMVRVVVVLVP 258
 QY 251 LTICFAPYVMTLAEI---VPFVTYNAQWGLSKCLTYSKAVADPFTYSL-----LRPFRQ 303
 Db 259 AGCWLPPFIVINVLAFALPEEPASAGLYFFVWLVSYNSCANPCLYGLFSLNLRQSPRK 318
 QY 304 VL 305
 Db 319 VL 320

RESULT 11

QYHY2 QYHY2 PRELIMINARY; PRT; 340 AA.
 AC QYHY2;
 DT 01-MAY-1999 (TREMELrel. 10, Created)
 DT 01-MAY-1999 (TREMELrel. 10, Last sequence update)
 DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
 DE Putative odorant receptor LOR14.
 OS Lampetra fluviatilis (River lamprey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
 OC Petromyzoniformes; Petromyzontidae; Lampetra.
 OX NCBI_TaxID=7748;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Olfactory organ;
 RA Berghard A., Dryer L.;
 RT "A novel family of ancient vertebrate odorant receptors";
 RL J. Neurobiol. 0:0-0(1998).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL; AF069548; AAC82383.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin...; IEA.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm1; 1.
 DR PRINTS; PR00237; GPCRHHODOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Receptor; Transmembrane.
 SQ SEQUENCE 340 AA; 37947 MW; E329864C73C18F25 CRC64;
 Query Match 12.4%; Score 229.5; DB 13; Length 340;
 Best Local Similarity 22.2%; Pred. No. 3.1e-11;
 Matches 74; Conservative 65; Mismatches 141; Indels 53; Gaps 9;
 QY 2 GRCEALLAGLLVMV-----LAVALLSNALVLLCCAYSALRTRASGVLLVNLSLGHLIA 56
 Db 23 GPTQVREVRVLLVIFAFPTITATILGNLLIITAIASFKYKLTQTHAN-FLAISLVSDLLVG 81
 QY 57 ALDMPFTLLGVNRGRTSPAGACQVIGFDTFLASNAALSVAALSDADQWLVAGFPLRYAG 116
 Db 82 VETMPLSMVKTYVDCWYFASVLCNARYFLDYTLTTATILHITCIAYDRYVAICDELRYAT 141
 QY 117 RLRPYAGLLGANGCSQSLAFSCAALGCSWLGYSAPASCRLRPPERPRFAAFTATL 176

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Db 142 RVTETIAALLVLCWGAIFSSPIL-----LSFSTLGRNIBRASCDDCVFVSFGIL 197
QY 177 HAUG---FVLPLAVLCSTSLQVHRVARRHCQMDVTVMKALLADLHPSVRQCLIQOK 233
Db 198 VTIVGPGPFTAHVVLVYVYVARRQSRKV-----AADSAVKQM 240
QY 234 RRRHRAIRKIGIAITFLICFAPYVWTLAE-----LVPFVTVNAQWGLSKCLTYSKA 287
Db 241 KREHSAAKTLGAIIGTFMLSPYVYVWVGFTVDGLFIPYRV--AMW-----IGYCSS 292
QY 288 VADPPTYSLRRPFR-----OVLAGMVHR 311
Db 293 AINPLLYASFNPFRTAFDFELRVFSGVVR 325

RESULT 12
Q9JK40
ID Q9JK40 PRELIMINARY; PRT; 385 AA.
AC Q9JK40;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Somatostatin subtype 5 receptor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/Sv;
RA O'Carroll A.-N.;
RT "Cloning, sequence and tissue distribution of the gene encoding a
mouse somatostatin subtype 5 receptor."
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR HSSP; P02699; 1F88.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0004872; F: receptor activity; IEA.
DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; 1.
DR PROSITE; PS00262; G-PROTEIN RECEPTOR FL2; 1.
DR G-protein coupled receptor; Receptor; Transmembrane.
KW SEQUENCE 385 AA; 42489 MW; 58C1140BF09FCEB5 CRC64;

Query Match 12.3%; Score 229; DB 11; Length 385;
Best Local Similarity 25.7%; Pred. No. 3.9e-11;
Matches 95; Conservative 53; Mismatches 162; Indels 60; Gaps 13;

QY 1 MGPGEALLAGLVVYLAVALLSNALVLLCCAYSAELTRASGVLLVNLGLHLLAALDM 60
Db 56 MGARAVLPVLYLVCTVGLGNTLVTVVRYAKMT-VTVNLMLVADVLF-MGL 113
QY 61 PFTLLGVNRGTPSAPGACQVIGFDLTFASNALSVAALSADQWLAVGFPLRYAGLRP 120
Db 114 PFLATQNAVSVYVPGSFCLRWLTLDGINQFTSFCLMWSVDYLAHVHPLRSARWRP 173
QY 121 RYAGLLGCANGOSLAFSGAALGCSWLGYSAPASCSRLPPEPRPFAAFTALHVG 180
Db 174 RVAKLASAAVWVFLMLSLPLL--VFADVQBGWGTCLNSW-PEPVGLWGAFTYTVSLG 230
QY 181 FVLPLAVLCSTSLQVHRVARRHCQMDVTVMKALLADLHPSVRQCLIQOKRRHRAT 240
Db 231 FFGPLLVLCL-----CVILLIVKYKAGMRV-----SSRR-----RSEKVT 269
QY 241 RKIGIAITFLICFAPYVWTLAE-----LVPFVTVNAQWGLSKCLTYSKAVADPFTYSL 297
Db 270 RMVYVVLVFGVCLPFPFIVNVLNLAFTLPPEPTAGLYFFVVVLSVANSANPLLYGFL 329

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QY 298 ----RRPFRQVLAGMVHRLKR-----TPRPASTHSDSLDVAGMVHQLKRTPRP 343
Db 330 SDNFRQSRKALC-----LRGYGVEDADALEPRD-----DKSGRPQTTL-----PTR 372
QY 344 ASTHNGSVDT 353
Db 373 SCEANGLMQT 382

RESULT 13
O42316
ID O42316 PRELIMINARY; PRT; 437 AA.
AC O42316;
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE DIA4 dopamine receptor.
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinus.
OX NCBI_TaxID=7962;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RX MEDLINE=99044151; PubMed=9826915;
RA Hirano J., Archer S.N., Djamgoz M.B.A.;
RT "Dopamine receptor subtypes expressed in vertebrate (carp and eel)
retinae: cloning, sequencing and comparison of five D1-like and three
D2-like receptors."
RT D2-like receptors."
RL Recept. Channels 5:387-404 (1998).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; Y14627; CAA74971.1; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0004872; F: receptor activity; IEA.
DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; 1.
DR PROSITE; PS00262; G-PROTEIN RECEPTOR FL2; 1.
DR G-protein coupled receptor; Receptor; Transmembrane.
KW SEQUENCE 437 AA; 48707 MW; A447494752139CE CRC64;

Query Match 12.3%; Score 228.5; DB 13; Length 437;
Best Local Similarity 22.3%; Pred. No. 4.9e-11;
Matches 74; Conservative 79; Mismatches 142; Indels 37; Gaps 13;

QY 7 LLAG-LLVMVLAVALLSNALVLLCCAYSAELTRASGVLLVNLGLHLLAALDMPFTLL 65
Db 22 VLTGCFSLILTLTLLGNTLVCAAVTKPRLRSKVTNPFVISLAISDLVAILVMPKAA 81
QY 66 GVMRGTPSAPGA-CQVIGFDLTFASNALSVAALSADQWLAVGFPLRYAGLRPRVAG 124
Db 82 SEIVGFWPF--GAFCDVWVAFDMCSTAILNLCVISVDRYWAISSPFRYERKMTPKVAF 139
QY 125 LLLGCANGOSLAFSGAALGCSWLGYSAPASCSRLPPEPRPFAAFTALHVG 181
Db 140 IMLSLAWTSLILSIPVQLNWHKQAQELNGTYGELPDNCDSSLNRYTATSSSL--ISF 197
QY 182 VLPLAVLCSTSLQVHRVARRHCQMDVTVMKALLADLHPSVRQCLIQOK-----R 234
Db 198 YIPVAILMVTYTRIYIAQKQIRISALE-RAAESAKNRHSHSMGNMNASWESSFMSFK 256
QY 235 RRHRAIRKIGIAITFLICFAPYVWTLAEVLPFVTVNAQWGLSKCLT----- 283
Db 257 RETKVLKLTUSVIMGVVCCWLEFFV--LNCWVPFCNPNE--GSDFFCISSTTFDFVWFG 312
QY 284 YSKAVADPFTYSL-----LRRPFRQVLAGMVHRL 312

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Db 313 WANSLSNPIIYAFNAGFRKAF-SILIG-CHRL 342

RESULT 14

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O9PVGO PRELIMINARY; PRT; 367 AA.
ID Q9PVGO
AC Q9PVGO
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Somatostatin receptor type 1 subtype A.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OC NCBI_TaxID=7957;
OX NCBI_TaxID=7957;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=20005543; PubMed=10537151;
RA Lin X., Janovick J.A., Brothers S., Conn P.M., Peter R.E.;
RT "Molecular cloning and expression of two type one somatostatin
RT receptors in goldfish brain."
RL Endocrinology 140:5211-5219(1999).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC EMBL; AF097726; AF08613.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 367 AA; 41658 MW; BE856C26C103614 CRC64;

Query Match 12.28; Score 227.5; DB 13; Length 367;
Best Local Similarity 23.04; Pred. No. 5e-11;
Matches 86; Conservative 75; Mismatches 160; Indels 53; Gaps 14;

QY 2 GPGEALAGLVLMVAVALLSNALVLLCCAYSAELRTRASGVLLVNLGLHLLAALDMP 61
Db 31 GSSAIFISFIYSVCLVGLCGNSWIVVIERAKMT-ATNIYILNLAIADELL-MSVP 88
QY 62 FTLLGVNRGRTAPGACQVIGFLDTFLASNAALSVAALSDQWLAVGFPLRYAGRLRP 121
Db 89 FLVTSLLHHWPFGLLCRLVLSVDAINMFTSIYCLTVLSDIYISVHPHKAARYRRPT 148
QY 122 YAGLLGCWAGQS-----LAFSGAALGCSWLGYSAFASCSRLRPPEPRFAAFTA 174
Db 149 IAKNVNLGVWVFSILVLPILIIISTAPN-----SDGSVACNMQM-PEPERQWAVFVI 201
QY 175 TLHAGVFLVPLAVCLFSLQVHRVARHCQMDVTVMKALLADLHPSVQRCLIQQR 234
Db 202 YAFLMGFLFPVIAICM-----CYILIIIVKRVVVALKAGNQ-----QRKK 240
QY 235 RHPRATKIGIAIATLFCFAPYVMTLAEIVPFTV-NAQWGLSKCLTYSKAVADPFT 293
Db 241 SERKITLVMVMVTVFVICWMPHIMGLSV-FVQOHNATLSQLAVILGYANSCANPIL 298
QY 294 YSLI-----RRPFRQVLAMVHRLKTRPRPASTHDSLSLVAG-MVHQLKTRPRPASTN 348
Db 299 YGFLSDNFRSFRILC-LRWMDNATEEPIDYATALKSRGYSVDDF-----OPENLES 351
QY 349 GSVDTENDSCLQQT 362
Db 352 GST-YRNGTCTSTRT 364
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RESULT 15

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O96716 PRELIMINARY; PRT; 391 AA.
ID O96716
AC O96716;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Dopamine D1/beta receptor.
OS Branchiostoma lanceolatum (Common lancelet) (Amphioxus).
OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OC Branchiostoma.
OC NCBI_TaxID=7740;
OX NCBI_TaxID=7740;
RN [1]
RP SEQUENCE FROM N.A.
RA Cardinaud B., Gibert JM., Sugamori K.S., Coudouel S., Guibert B.,
RA Vincent J.D., Niznik H.B., Vernier P.;
RT "The amphioxus D1/beta receptor and the emergence of the vertebrate
RT adrenergic system."
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC EMBL; AJ005433; CAA06536.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 391 AA; 42622 MW; 67A5AD944AFA3FBE CRC64;

Query Match 12.28; Score 227.5; DB 5; Length 391;
Best Local Similarity 20.98; Pred. No. 5.3e-11;
Matches 77; Conservative 80; Mismatches 159; Indels 53; Gaps 12;

QY 5 BALLAGLLVMVAVALLSNALVLLCCAYSAELRTRASGVLLVNLGLHLLAALDMPFTL 64
Db 39 QAVLGLITVILLITLVIGNVILAVTCHRMRT-VTNFFIVSLACADLSVGITVLPFAA 97
QY 65 LGVMRGRTSPAGACQVIGFLDTFLASNAALSVAALSDQWLAVGFPLRYAGRLRPYAG 124
Db 98 TNDILGVWPFQ-GYCDVWVSFDVNLSTASILNLVVIADFRLAITAPFTYHTRWERTAG 156
QY 125 LLLGCWAGQS-LAFSGAALGCSWLGYSAFASCSRLRPPEPRPF---AAFTATLHAGVF 181
Db 157 ILIATVWGISLVWVSLPIQAGW--YRDNQSEALAIYSDPCLCIFTASTAYTIVSSLSIF 214
QY 182 VPLAVLCLTSQVHRVARHCQMDVTVMKALLADLHPSVQRCLIQQR-----236
Db 215 YIPLILMLVFYGIIFKAARDQARKINALEGR-----LSENNRGKKIS 257
QY 237 ---HRATRKIGIAIATLFCFAPYVMTLAE-----LVPFVTVNAQW-GILSKCLTY 285
Db 258 LAKEKAAKTGLIIMGVIFILCMFPFVNVINVPFCDCVQPAVFIALTWLWINSCE---314
QY 286 KAVADPFTYSLRPPFRQVLAGNV--HRLKTRPRPASTHDSLSLVAGMVHQLKTRPRP 343
Db 315 ---NPIIYA-FNKEFRKVFVKMICCHKRCRGVTGVP---NHADLNYPFVAMRLKRGENA 366
QY 344 ASTNGSVVD 352
Db 367 NGTVNGDAN 375
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Search completed: May 18, 2004, 12:08:08

Job time : 48 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: May 18, 2004, 12:06:02 ; Search time 22 Seconds
(without alignments)
851.829 Million cell updates/sec

Title: US-10-049-569-2
Perfect score: 1858
Sequence: 1 MGPGEALLAGLLVMYLAVAL.....ASTHNGSVDTENDSCLQOTH 363

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	848	45.6	337	2	US-09-013-634-2
2	236	12.7	348	3	US-08-875-540-13
3	236	12.7	348	4	US-09-171-456-17
4	236	12.7	348	4	US-09-473-634-13
5	232.5	12.5	359	2	US-08-748-485-5
6	232.5	12.5	391	3	US-08-120-601B-8
7	230.5	12.4	402	1	US-08-444-734A-6
8	230.5	12.4	402	1	US-08-087-772A-15
9	230.5	12.4	402	3	US-08-846-704-4
10	230.5	12.4	408	1	US-07-916-901-2
11	230.5	12.4	408	3	US-08-450-962-2
12	230.5	12.4	408	3	US-08-450-962-5
13	230.5	12.4	408	4	US-08-848-631-2
14	230.5	12.4	408	4	US-08-848-631-5
15	230.5	12.4	425	4	US-09-479-128-2
16	229.5	12.4	402	4	US-08-463-509B-2
17	229.5	12.4	402	5	PCT-US95-05616-2
18	229.5	12.4	425	3	US-08-846-704-2
19	229.5	12.4	425	4	US-09-211-823C-22
20	228.5	12.3	391	1	US-07-816-283-2
21	228.5	12.3	391	1	US-07-816-283-4
22	228.5	12.3	391	1	US-08-417-103-2
23	228.5	12.3	391	1	US-08-417-103-4
24	228.5	12.3	391	1	US-08-417-103-14
25	228.5	12.3	477	1	US-07-791-936A-2
26	228.5	12.3	477	1	US-08-383-781B-2
27	228.5	12.3	477	2	US-07-969-267B-2

28	228.5	12.3	477	4	US-09-168-510-2	Sequence 2, Appli
29	228	12.3	385	4	US-08-981-700A-4	Sequence 4, Appli
30	228	12.3	387	3	US-08-993-088A-7	Sequence 7, Appli
31	228	12.3	387	4	US-08-993-424B-7	Sequence 7, Appli
32	228	12.3	387	4	US-09-595-549-10	Sequence 10, Appli
33	228	12.3	387	4	US-09-603-680-7	Sequence 7, Appli
34	228	12.3	387	4	US-08-899-112B-28	Sequence 28, Appli
35	228	12.3	475	1	US-07-686-591-4	Sequence 4, Appli
36	228	12.3	475	1	US-07-970-715-4	Sequence 4, Appli
37	227.5	12.2	408	1	US-08-351-473B-3	Sequence 3, Appli
38	226.5	12.2	359	2	US-08-103-170-4	Sequence 4, Appli
39	226.5	12.2	359	2	US-08-103-170-6	Sequence 6, Appli
40	226.5	12.2	400	2	US-08-103-170-9	Sequence 9, Appli
41	226	12.2	353	2	US-08-467-559B-10	Sequence 10, Appli
42	225.5	12.1	365	2	US-08-428-243-9	Sequence 9, Appli
43	225.5	12.1	365	5	PCT-US93-10301-9	Sequence 9, Appli
44	224	12.1	369	3	US-08-120-601B-9	Sequence 8, Appli
45	224	12.1	372	2	US-08-626-685A-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-09-013-634-2
; Sequence 7, Application US/08991946A
; Patent No. 5945306
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Tang, Tom Y.
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: RAS PROTEINS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/991.946A
; FILING DATE: December 16, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cerrone, Michael C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0445 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; Sequence 2, Application US/09013634
; Patent No. 5945307
; GENERAL INFORMATION:
; APPLICANT: M. Alexandra Glucksmann and Keith Robison

;/ TITLE OF INVENTION: LIGAND RECEPTORS AND USES THEREFOR
;/ NUMBER OF SEQUENCES: 14
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: LAHIVE & COCKFIELD, LLP
;/ STREET: 28 State Street
;/ CITY: Boston
;/ STATE: Massachusetts
;/ COUNTRY: USA
;/ ZIP: 02109
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: Patent in Release #1.0, Version #1.25
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/09/013,634
;/ FILING DATE:
;/ CLASSIFICATION:
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER:
;/ FILING DATE:
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Attorney, Jean M. Silveri
;/ REGISTRATION NUMBER: 39,030
;/ REFERENCE/DOCKET NUMBER: MWI-036
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (617)227-7400
;/ TELEFAX: (617)742-4214
;/ INFORMATION FOR SEQ ID NO: 2:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 337 amino acids
;/ TYPE: amino acid
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: protein
;/ US-09-013-634-2

Query Match 45.6%; Score 848; DB 2; Length 337;
Best Local Similarity 52.0%; Pred. No. 9.6e-66;
Matches 170; Conservative 52; Mismatches 101; Indels 4; Gaps 1;
QY 1 MCGEALLAGLVVLAVALLSNALVLTCCAYSAELRTRASGVLLVNLGLHLLAALDM 60
DB 1 MNSWDAGLAGLVGTGVSLSNALVLLCLLHSDIRQAPALTEMLTGNLCTVNM 60
QY 61 PFTLLGVNMGRTSPAGCAQVIGFDTFLASNAALSVAALSADQWLAGVFPRLYAGRLRP 120
DB 61 PLTLAGVVARQPDGRLCRLAAFLDTFLAANSMLSAALSIDRWAVVFPVSYAKWRL 120
QY 121 RVAGLLGCWGQSLAFSGAALGCSWLGYSYSAFASCSRLPPEPRPFAAFTATLHVG 180
DB 121 RDAALMVAYTWLHALTTPAALALSGLWLGHQYASCTLCSSRRPDERLRFVFTGAFHALS 180
QY 181 FVLPLAVLCLTSLOVHRVARHRCQMDVTVMKALLADLHPSVRQRCCLIOQKRRHRAT 240
DB 181 FLLSFVLCCTYLVKLVARHCKRIDVTWQTLVLLVDLHPSVRERCLBEQKRRQRAT 240
QY 241 RKIGIAIAATFLICFAPYVMTLAEVFPVTVNAQWGLSKCLITYSKAVADPFTYLLRRP 300
DB 241 KKISTFICTFLVCFAPYVITRIVELFSTVPIGSHWGLSKCLAYSKAASDPFVYSLRHQ 300
QY 301 FQVLGAVVHRLKTRTPASTHDSLL 327
DB 301 YKSKCEILNRLHR-----RSIHSSGL 323

RESULT 2
US-08-875-540-13
; Sequence 13, Application US/08875540A
; Patent No. 6015888
; GENERAL INFORMATION:
; APPLICANT: Heath, Paul Roy
; APPLICANT: Orange, Paul Richard
; APPLICANT: Pearson, Ronald Carl Alan

;/ APPLICANT: Wright, Simon Ralph
;/ TITLE OF INVENTION: IMPROVEMENTS IN OR RELATING TO THE DETECTION OF VARIATIONS IN
;/ FILE REFERENCE: 09347/002001
;/ CURRENT APPLICATION NUMBER: US/08/875,540A
;/ CURRENT FILING DATE: 1998-01-05
;/ EARLIER APPLICATION NUMBER: PCT/EP96/00397
;/ EARLIER FILING DATE: 1997-01-30
;/ EARLIER APPLICATION NUMBER: GB9503866.7
;/ EARLIER FILING DATE: 1995-01-30
;/ NUMBER OF SEQ ID NOS: 15
;/ SOFTWARE: FastSeq for Windows Version 3.0
;/ SEQ ID NO. 13
;/ TYPE: PRT
;/ LENGTH: 348
;/ ORGANISM: Homo sapiens
;/ US-08-875-540-13

Query Match 12.7%; Score 236; DB 3; Length 348;
Best Local Similarity 24.1%; Pred. No. 9.8e-13;
Matches 85; Conservative 60; Mismatches 146; Indels 62; Gaps 11;
QY 12 LVNVLAVALL-----SNALVLLCCAYSAELRTRASGVLLVNLGLHLLAALDMPTLLGV 67
DB 18 ITVVLAVLILITVAGNVVVCVLAAGLNRRLR- NLTCFIVSLAITDLLGLLVLPFSAIYQ 76
QY 68 MGRTPSAPGACQVIGFDTFLASNAALSVAALSADQWLAGVFPRLYAGRLRPYAGLLL 127
DB 77 LSKWMSFGKVCNIYVTSLDVMLCTASILNLFMISLDRCVAMDFLRYVLTVPARVAISL 136
QY 128 GCWQSLAFSGAALGCSWLGYS-----APASGLRLPPEPRPFAAFTATLHVG 181
DB 137 VLIWVISITLSFLSIHLGWSNRNETSKGNHTTKCNVQV-----EYGLVDGLVTF 188
QY 182 VLPLAVLCLTSLOVHRVARHRCQMDVTVMKALLADLHPSVRQRCCLIOQKRRHRAT 241
DB 189 YLPLLMICITYYRIFKAVDQAKRIDHISWKAAT-----REHRAV 231
QY 242 KIGIAIAATFLICFAPYVMTLAEVFPV-----TVNAQWGLSKCLITYSKAVADPFT 293
DB 232 TLAAVMGAFIICWFPY-----FTAFVYVGLRGDDAINEMLEAIVLWLGYSANALNPIL 284
QY 294 YSLLRPFR---OVLGAVVHRLKTRTPASTHDSLL-DVAGMVHQLKTRTP 342
DB 285 YAALNRDFTGYCQL--FCCLANR-----NSHKTSLSRNASQLSRTQSTQREPR 330

RESULT 3
US-09-171-456-17
; Sequence 17, Application US/09171456A
; Patent No. 6346380
; GENERAL INFORMATION:
; APPLICANT: Wright, Simon Ralph
; APPLICANT: Heath, Paul Roy
; APPLICANT: Orange, Paul Richard
; APPLICANT: Pearson, Ronald Carl Alan
;/ TITLE OF INVENTION: DETECTION OF VARIATIONS IN HUMAN H2 RECEPTORS
;/ FILE REFERENCE: 09347/004001
;/ CURRENT APPLICATION NUMBER: US/09/171,456A
;/ CURRENT FILING DATE: 1999-08-03
;/ EARLIER APPLICATION NUMBER: PCT/GB97/01075
;/ EARLIER FILING DATE: 1997-04-18
;/ NUMBER OF SEQ ID NOS: 19
;/ SOFTWARE: FastSeq for Windows Version 4.0
;/ SEQ ID NO. 17
;/ LENGTH: 348
;/ TYPE: PRT
;/ ORGANISM: Homo sapiens
;/ US-09-171-456-17

Query Match 12.7%; Score 236; DB 4; Length 348;
Best Local Similarity 24.1%; Pred. No. 9.8e-13;
Matches 85; Conservative 60; Mismatches 146; Indels 62; Gaps 11;

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QY 12 LVNVLAVALL-----SNALVLLCCAYSABELTRASGVLLVNLISLGHLLAALDMPFTLLGV 67
DB 18 ITVVLAVLITVAGNVVCLAVGLNRRL-NLTCFIVSLAITDILLGLLVLPSAIYQ 76
QY 68 MRGRTPSAPGACQVIGFLDTFFLASNAALSVAALSADQWLAVGFFPLRYAGRLRPYAGLL 127
DB 77 LSCKWSFGKVFVFCNIYTSLDVMLCTASILNLFMISLDRYCAVMDPLRYPLVTPARVAISL 136
QY 128 GCAGGSLAFSGAALGCSMLGYSS-----AFASCSRLRPPPERPFAAFTATLHAYGVF 181
DB 137 VLIWVISITLSFSLHGLWNSRNETSKGNHTTSKCNQVN-----EYGLVDGLVTF 188
QY 182 VLPLAVLCLTSLQVHVARHCOQMDVTVMKALALLADLHPSVORCLIQOQRHRRATR 241
DB 189 YLPLLMICITYYRIFRVARDOAKRIDHISSWKAATI-----REHRAIV 231
QY 242 KIGIATATFLICFAPYVWTRLAELVPFV-----TVNAQWGLSKCLITYSKAVADPFT 293
DB 232 TLAAVMGAFIICWFFY-----FTAFVYRGLRGDDAINEMLEAIVLWLGANSALNPIL 284
QY 294 YSLRRPFR---QVLAGMVHRLKRTPRPASTHDSLS-DVAGMVHQLLKRTPR 342
DB 285 YAALNRDFTGYQOL--FCRLANR-----NSHKTSLRNSAQLSRTQSREPR 330

RESULT 4
US-09-473-634-13
; Sequence 13, Application US/09473634
; Patent No. 6440670
; GENERAL INFORMATION:
; APPLICANT: Heath, Paul Roy
; APPLICANT: Orange, Paul Richard
; APPLICANT: Pearson, Ronald Carl Alan
; APPLICANT: Wright, Simon Ralph
; TITLE OF INVENTION: IMPROVEMENTS IN OR RELATING TO THE DETECTION OF VARIATIONS IN
; FILE OF INVENTION: HUMAN HISTAMINE H2 RECEPTORS
; FILE REFERENCE: 09347/002001
; CURRENT APPLICATION NUMBER: US/09/473,634
; CURRENT FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: US 08/875,540
; PRIOR FILING DATE: 1998-01-05
; PRIOR APPLICATION NUMBER: PCT/EP96/00397
; PRIOR FILING DATE: 1997-01-30
; PRIOR APPLICATION NUMBER: GB9503866.7
; PRIOR FILING DATE: 1995-01-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 348
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-473-634-13

Query Match 12.7%; Score 236; DB 4; Length 348;
Best Local Similarity 24.1%; Pred. No. 9.8e-13;
Matches 85; Conservative 60; Mismatches 146; Indels 62; Gaps 11;

QY 12 LVNVLAVALL-----SNALVLLCCAYSABELTRASGVLLVNLISLGHLLAALDMPFTLLGV 67
DB 18 ITVVLAVLITVAGNVVCLAVGLNRRL-NLTCFIVSLAITDILLGLLVLPSAIYQ 76
QY 68 MRGRTPSAPGACQVIGFLDTFFLASNAALSVAALSADQWLAVGFFPLRYAGRLRPYAGLL 127
DB 77 LSCKWSFGKVFVFCNIYTSLDVMLCTASILNLFMISLDRYCAVMDPLRYPLVTPARVAISL 136
QY 128 GCAGGSLAFSGAALGCSMLGYSS-----AFASCSRLRPPPERPFAAFTATLHAYGVF 181
DB 137 VLIWVISITLSFSLHGLWNSRNETSKGNHTTSKCNQVN-----EYGLVDGLVTF 188
QY 182 VLPLAVLCLTSLQVHVARHCOQMDVTVMKALALLADLHPSVORCLIQOQRHRRATR 241
DB 189 YLPLLMICITYYRIFRVARDOAKRIDHISSWKAATI-----REHRAIV 231

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QY 242 KIGIATATFLICFAPYVWTRLAELVPFV-----TVNAQWGLSKCLITYSKAVADPFT 293
DB 232 TLAAVMGAFIICWFFY-----FTAFVYRGLRGDDAINEMLEAIVLWLGANSALNPIL 284
QY 294 YSLRRPFR---QVLAGMVHRLKRTPRPASTHDSLS-DVAGMVHQLLKRTPR 342
DB 285 YAALNRDFTGYQOL--FCRLANR-----NSHKTSLRNSAQLSRTQSREPR 330

RESULT 5
US-08-748-485-5
; Sequence 5, Application US/08748485
; Patent No. 5817480
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Guegler, Karl J.
; APPLICANT: Goli, Surya K.
; APPLICANT: Murty, Lynn E.
; TITLE OF INVENTION: NOVEL HISTAMINE H2 RECEPTOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/748,485
; FILING DATE: Herewith
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0159 US
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 791239
US-08-748-485-5

Query Match 12.5%; Score 232.5; DB 2; Length 359;
Best Local Similarity 22.0%; Pred. No. 2e-12;
Matches 73; Conservative 67; Mismatches 139; Indels 53; Gaps 8;

QY 11 LLNVLAVALLSNALVLLCCAYSABELTRASGVLLVNLISLGHLLAALDMPFTLLGVNRG 70
DB 24 ILIILITVAGNVVCLAVGLNRRLAS-LTNCFTIVSLAVTDLLGLLVLPSAIYQLSC 82
QY 71 RTPAPGACQVIGFLDTFFLASNAALSVAALSADQWLAVGFFPLRYAGRLRPYAGLLGCA 130
DB 83 KWSFKVFCNIYTSLDVMLCTASILNLFMISLDRYCAVTDPLRYPLVTPARVAISLVI 142
QY 131 WQGSFLAFSGAALGCSMLGY-----SSAFASCSRLRPPPERPFAAFTATLHAYGVLP 184

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Db 143 WVISTLSFLSIHLGWSRNETSKDNTIVKCKQVNN-----EVYGLVDGLVTYFLP 194
QY 185 LAVCLTSLQVHRVARHCQMDTV-TWKALALLADLHPSVRQCLIQKKRRHRATRKI 243
Db 195 LLIMCITYFRIFKIAREQARRINHGSKAATI-----REHKATVTL 236
QY 244 GIAIATFLICFAPYVMTLAEVLV-----TVNAQWGLSKCLTYKAVADPTYS 295
Db 237 AAVMGAFICFPY-----FTVYVYGLKGDADVNEFEDVVLWLGYSALNPLIYA 289
QY 296 LLRRPFRQVLGAMVHRLKTRTPASTHSSSL 327
Db 290 ALNRDRTA---YHOLFCCRLASHNSHETSLSL 317
RESULT 6
US-08-120-601B-8
; Sequence 8, Application US/08120601B
; Patent No. 6235496
; GENERAL INFORMATION:
; APPLICANT: Yu, Lei
; TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND
; METHODS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/120,601B
; FILING DATE: 13-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: INDA:002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 391 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-120-601B-8
Query Match 12.5%; Score 232.5; DB 3; Length 391;
Best Local Similarity 24.5%; Pred. No. 2.3e-12;
Matches 78; Conservative 62; Mismatches 130; Indels 49; Gaps 11;
QY 2 GPGEALLAGLVVLA-VALLSNALVLLCCAYSALRTRASGVLLVNLGLHLLAALDM 60
Db 54 GQGSAILISFIYSVCLVGLCGNSMVIYVILRYAKMT-ATNIVILNLAIDELL-MLSV 111
QY 61 PFTLLGVNRGTPSAPGACOVIGFLDTFLASNAALSVAALSADQWLAVGFLRYAGLRP 120
Db 112 PELVTSTLLRHWFPGALLCRLVSLVDAYNMTSIVCLTVLSVDVRYAVVHPKAAVRRP 171
QY 121 RVAGLLLCGAWQS-----AFGGAALGCSWLGYSASFASLSRLRPPPEPRPRAFT 173
Db 172 TVAKVNLGVWVLSLVILPIVVFERTAN-----SDGTVACNM-LMPEPAQRWLGVFV 224
QY 174 ATLHAGVFLPLAVTCLTSLQVHRVARHCQMDTVTWKALALLADLHPSVRQCLIQOK 233

Db 225 LVTFMGFLPLVGAICL-----CYVLIATKQWVVALKAGWQ-----QEK 263
QY 234 RRRHRATRKIGIAIATFLICFAPYVMTLAEVLV-----PFTVNAQWGLSKCLTYKAVAD 290
Db 264 RSRKITTLMVMVMVVFVICWMPFVYVQVNVFAEQDDATVSQ-----LSVILGYANSCAN 319
QY 291 PFTYSLL-----RRPFRVL 305
Db 320 PLYGLFSLDNFRSFQRI 338
RESULT 7
US-08-444-734A-6
; Sequence 6, Application US/08444734A
; Patent No. 5610282
; GENERAL INFORMATION:
; APPLICANT: Sibley, David R.
; APPLICANT: Monsma, Frederick J.
; APPLICANT: Mahan, Lawrence C.
; APPLICANT: McVittie, Loris D.
; TITLE OF INVENTION: cDNA encoding the rat D1 dopamine
; receptor linked to adenylyl cyclase activation and
; TITLE OF INVENTION: expression of the receptor protein in plasmid-transfected
; TITLE OF INVENTION: cell lines
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson and Bear
; STREET: 620 Newport Center Drive, Sixteenth Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92560
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,734A
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/029,917
; FILING DATE: 03-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/548,714
; FILING DATE: 06-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E.
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: NIH065.001FWI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (714) 760-0404
; TELEFAX: (714) 760-9502
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 402 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
US-08-444-734A-6
Query Match 12.4%; Score 230.5; DB 1; Length 402;
Best Local Similarity 24.9%; Pred. No. 3.5e-12;
Matches 93; Conservative 61; Mismatches 154; Indels 65; Gaps 14;
QY 3 PGEALLAGLVVLAVALIS-----NALVLLCCAYSALRTRASGVLLVNLGLHLLAAL 58
Db 34 PWEALAGAL---LALAVLATVGGNLLVIVATWPRLOT-MTNVFTVSLAADLVMGIL 89

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QY 59 DMPFTLLGVNRGTPSPAGACQVIGFLDTFLASNAALSVAALSADQWLAVGFLRYAGRL 118
DB 90 WVPAAATLALTGHWPFGATGCELWTSVDVLCVTASITETLCALAVDRYLAVTNPLRYGALV 149
QY 119 RPYAGLLGCAWGQSLATSGAALGCSW--LGYSSAFASCSLRLPPEPRPFAAFTATL 176
DB 150 TKKARTAVVLVWVSAVSPFAPIMSQWVRVGDAAEQCH-----SNPRCCAFASNM 202
QY 177 -----HAGVFVPLAVLCLTSLQVHRVARRHC-----QMDTVMKALA--- 215
DB 203 PYVLLSSVSFYLPLVWLFVYARFVVAQRLRLRGELGRFPPEPPAPSRSLAPAP 262
QY 216 ----LLADLHPSVRORCLIOQKRRHRATKIGIAIATFLICFAPYVWTRL-----AEL 265
DB 263 VGTCAPEGVACGRPARLLPLREHRLCTGLINGTFTLCWLPFLANVLALGGPSL 322
QY 266 VP---FVTVAQWGLSKCLTYSKAVADPFTYSL---LRRPFQVLAGMVHRLKRTPRP 319
DB 323 VGPAPFALN--W-----LGYNSAFNPLIYCRSPDPSAFRLLCRCRRRL---PPEP 371
QY 320 ASTHDSLDVAGM 332
DB 372 CAARPALFPFSGV 384

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RESULT 8

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US-08-087-772A-15
; Sequence 15, Application US/08087772A
; Patent No. 5691155
; GENERAL INFORMATION:
; APPLICANT: Namias, Clara
; APPLICANT: Emorine, Jean L.
; APPLICANT: Strosberg, Donny A.
; TITLE OF INVENTION: Nucleotide Sequences Encoding the Murine
; TITLE OF INVENTION: Beta3-Adrenergic Receptor and Their Applications
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bell, Seltzer, Park & Gibson
; STREET: Post Office Drawer 34009
; CITY: Charlotte
; STATE: No. 5691155th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/087,772A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Linker, Raymond O.
; REGISTRATION NUMBER: 26,419
; REFERENCE/DOCKET NUMBER: 3339-195
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-881-3140
; TELEFAX: 919-881-3175
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 402 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-087-772A-15

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Query Match      12.4%; Score 230.5; DB 1; Length 402;
Best Local Similarity 24.9%; Pred No. 3,5e-12;
Matches 93; Conservative 61; Mismatches 154; Indels 65; Gaps 14;

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QY 3 PGEALLAGLVMVLAVALLS-----NALVLCCAYSAELRTRASGVLLVNLSLGHLILAAL 58
DB 34 PWEAALAGAL--LALAVLATVGNLLVIVAIATWPLRQT-MTNVFTSLAADLVNGLL 89
QY 59 DMPFTLLGVNRGTPSPAGACQVIGFLDTFLASNAALSVAALSADQWLAVGFLRYAGRL 118
DB 90 WVPAAATLALTGHWPFGATGCELWTSVDVLCVTASITETLCALAVDRYLAVTNPLRYGALV 149
QY 119 RPYAGLLGCAWGQSLATSGAALGCSW--LGYSSAFASCSLRLPPEPRPFAAFTATL 176
DB 150 TKKARTAVVLVWVSAVSPFAPIMSQWVRVGDAAEQCH-----SNPRCCAFASNM 202
QY 177 -----HAGVFVPLAVLCLTSLQVHRVARRHC-----QMDTVMKALA--- 215
DB 203 PYVLLSSVSFYLPLVWLFVYARFVVAQRLRLRGELGRFPPEPPAPSRSLAPAP 262
QY 216 ----LLADLHPSVRORCLIOQKRRHRATKIGIAIATFLICFAPYVWTRL-----AEL 265
DB 263 VGTCAPEGVACGRPARLLPLREHRLCTGLINGTFTLCWLPFLANVLALGGPSL 322
QY 266 VP---FVTVAQWGLSKCLTYSKAVADPFTYSL---LRRPFQVLAGMVHRLKRTPRP 319
DB 323 VGPAPFALN--W-----LGYNSAFNPLIYCRSPDPSAFRLLCRCRRRL---PPEP 371
QY 320 ASTHDSLDVAGM 332
DB 372 CAARPALFPFSGV 384

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RESULT 9

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US-08-846-704-4
; Sequence 4, Application US/08846704
; Patent No. 6020157
; GENERAL INFORMATION:
; APPLICANT: BERGSM, DEREK J.
; APPLICANT: ELLIS, CATHERINE E.
; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P. O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/846,704
; FILING DATE: 30-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 402 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-846-704-4

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Query Match 12.4%; Score 230.5; DB 3; Length 402;
Best Local Similarity 25.3%; Pred. No. 3.5e-12;
Matches 94; Conservative 55; Mismatches 154; Indels 69; Gaps 13;

QY 5 EALLAGLLVMVLAVALISNALVILCCAYSAEIRTRASGVLLVNLISLGHLLAALDMPFTL 64
DB 46 EWLIIAAVVAVFVALVGNLTUCLAVRNHHMRT-VNYFIYNLSLADVLVTAICLPASL 104
QY 65 LGVMRGRTSPAGACQVIGFDLDTFLASNAALSVAALSADQWLAVGVFLRYAGRLRPYAG 124
DB 105 LVDITESWLFCHALKVPIYLAQVSVVAVLTSLFIALDRWYAIHLLFKSTAR-RARG 163
QY 125 LLIGCANGQSIAFGAALGCSWLGVSFAFASCSRLPPEPERPFAA-----FTA 174
DB 164 SILG-INAVSLAI-----MVPQAAMVCSVLPPELANRTRKLFVCDERWADDLYPK 213
QY 175 TLHAGFVLP-LAVLCITSLQVHRVARRHCORMDVTVMKALA-----LLADL----- 220
DB 214 IYHSCFFIVTYLAPLGLMAMAYFOIFKLGWQIQPGTTSALVRNWKPSQDGLDLEGLS 273
QY 221 -HPSVROSL---IQKRRHRATRKIGIAIATFLICFAP-----YVMTRLA--- 263
DB 274 GEPQPRARAFIAEVKQKRAKTKAMLMVLLVFPALCYLPSVLNVLKRVFGMFRQASDR 333
QY 264 ELVFPVTNQAOWGILSKCLTYSKAVADPFTYSLRRPQVLI-----AGWVHRL 313
DB 334 BAVYACFTFSHW-----LVTANSANPIIYNFLSGKFRQFKAAPSCCLPGLGPCSLK 387
QY 314 KRTPRPASTHDS 325
DB 388 APSRSSASHKS 399

RESULT 10

US-07-916-901-2
; Sequence 2, Application US/07916901
; Patent No. 5364772
; GENERAL INFORMATION:
; APPLICANT: Granneman, James G.
; APPLICANT: Zahners, Kristine N.
; APPLICANT: Rao, Donald D.
; TITLE OF INVENTION: @ @3-ADRENERGIC RECEPTOR PROTEIN AND DNA
; TITLE OF INVENTION: ENCODING SAME
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: REISING, ETHINGTON, BARNARD, PERRY &
; ADDRESSEE: MILTON
; STREET: 201 W. Big Beaver - Ste. 400; P.O. Box 4390
; CITY: Troy
; STATE: Michigan
; COUNTRY: USA
; ZIP: 48099
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/916,901
; FILING DATE: 19920720
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,955
; REFERENCE/DOCKET NUMBER: P-324 (WSU)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (313) 689-3554
; INFORMATION FOR SEQ ID NO. 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 408 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear

MOLECULE TYPE: protein
US-07-916-901-2

Query Match 12.4%; Score 230.5; DB 1; Length 408;
Best Local Similarity 24.9%; Pred. No. 3.5e-12;
Matches 93; Conservative 61; Mismatches 154; Indels 65; Gaps 14;

QY 3 PGEALLAGLLVMVLAVALIS-----NALVLLCCAYSAEIRTRASGVLLVNLISLGHLLAAL 58
DB 34 PWEAALAGAL---LALAVLATVGGNLLVIVAIAMTPRLQT-MTNVFTVTSLAADLVNGLL 89
QY 59 DMPEFTLLGMRGRTSPAGACQVIGFDLDTFLASNAALSVAALSADQWLAVGVFLRYAGRL 118
DB 90 VVPPRAATLALGHWPGLGATGELTSDVLCTASIEITLCALAVDRYLAVTNPLRYGALV 149
QY 119 RPYRAGLLGCAWGQSIAFGAALGCSW--LGYSFAFASCSRLPPEPERPFAAFTATL 176
DB 150 TKRCARTAVLVVVVSAASVAFAPIMSQWVRVGADEAQAORCH-----SNPRCCAFASNM 202
QY 177 -----HAGFVLP-LAVLCITSLQVHRVARRHC-----QRMDDVTVMKALA--- 215
DB 203 PTVLLSSVSFVLPVLLVNLVFFVAVFVTVATRLRLRGELGRFPPEPSPPAPSRLAPAP 262
QY 216 ----LLADLHPSVRQRCILQKRRHRATRKIGIAIATFLICFAPYVMTRL-----AEL 265
DB 263 VGTCAPEGVGPACGRPARLLPLREHRACTLGLIMGTFTLCWLPFFFLANVLRALGGPSL 322
QY 266 VP---FVTVNQAOWGILSKCLTYSKAVADPFTYSL---LRRPFRQVLAGWVHRLKTRPP 319
DB 323 VEGPAFLALN--W-----LGYSANFNLPLYCRSPDFRSAPRRLLCGRRL-----PPEP 371
QY 320 ASTHDSLSLDVAGM 332
DB 372 CAARPALFPFSGV 384

RESULT 11

US-08-450-962-2
; Sequence 2, Application US/08450962
; Patent No. 6274706
; GENERAL INFORMATION:
; APPLICANT: EMORINE, Laurent; MARULLO, Stefano;
; APPLICANT: STROBERG, Donny
; TITLE OF INVENTION: INTRON/EXON OF THE HUMAN AND
; TITLE OF INVENTION: GENES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KECK, MAHIN & CATE
; STREET: P.O. BOX 06110
; CITY: CHICAGO
; STATE: ILLINOIS
; COUNTRY: U.S.A.
; ZIP: 60606-0110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3-1/2" diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,962
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/117,829
; FILING DATE: 08-SEPT-1993
; APPLICATION NUMBER: 07/721,571
; FILING DATE: 25-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR89/00918
; FILING DATE: 25-JAN-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Fleit, Martin; Gollin, Michael A.
; REGISTRATION NUMBER: 16,900; 31,957

REFERENCE/DOCKET NUMBER: 47078-042
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 789-3400
TELEFAX: (202) 789-1158
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 408 residues
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: polypeptide
US-08-450-962-2

Query Match 12.4%; Score 230.5; DB 3; Length 408;
Best Local Similarity 24.9%; Pred. No. 3.5e-12;
Matches 93; Conservative 61; Mismatches 154; Indels 65; Gaps 14;
QY 3 PGEALLAGLLVMVLAVALLS-----NALVLLCCAYSAELRTRASGVLLVNLGLHLLAAL 58
DB 34 PWEAALAGAL---LALAVLATVGGNLLVIVAIATWTPRLQT-MTNVFTSLAAADLVMGLL 89
QY 59 DMPFTLLGVNMGRTSPAGCQVIGFLDTFLASNAALSVAALSADOMLAVGFLRYAGRL 118
DB 90 VVPPAATLALTGHWPGLGATGCELWTSVDVLCVTSIETLCALAVDRYLAVTNPLRYGALV 149
QY 119 RPRVAGLLGCAGWSLAFSGAALGCSW--LGYSSAFASCSLRLPPEPRPFAAFTATL 176
DB 150 TKRCARTAVLVVWVSAVSPAPIMSQWVGVADAEARQCH-----SNPRCCAFASNM 202
QY 177 -----HAGFVLPLAVCLTSLQVHRVARHC-----QRMDTVTMKALA--- 215
DB 203 PYVLLSSVSFYLLVMLFVYARVFWATQRLRLGELGRFPPEESPAPSRSLAPAP 262
QY 216 ----LLADLHPSVRQCLTQKRRHRATKIGIAIATFLICFAPYVMTL-----AEL 265
DB 263 VGTCAPEGVACGRPARLLPLREHRLCTGLINGTFLCWLFFFLANVLALGGPSL 322
QY 266 VP---FVTNAGWILSKCLTYSKAVADPFTYSL---LRRPFRQVLAVGWHRLKRTPRP 319
DB 323 VPGPAFLALN--W-----LGYANSAFNPLIYCRSPDFRSAPFRLLRCGRRL---PPEP 371
QY 320 ASTHDSLDVAGM 332
DB 372 CAARPALEPESGV 384

RESULT 12
US-08-450-962-5
Sequence 5, Application US/08450962
Patent No. 6274706
GENERAL INFORMATION:
APPLICANT: EMORINE, Laurent; MARULLO, Stefano;
APPLICANT: STROBERG, Donny
TITLE OF INVENTION: INTRON/EXON OF THE HUMAN AND
TITLE OF INVENTION: GENES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: KECK, MAHIN & CATE
STREET: P.O. BOX 06110
CITY: CHICAGO
STATE: ILLINOIS
COUNTRY: U.S.A.
ZIP: 60606-0110
COMPUTER READABLE FORM:
MEDIUM TYPE: 3-1/2" diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,962
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/117,829
FILING DATE: 08-SEPT-1993
APPLICATION NUMBER: 07/721,571
FILING DATE: 25-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR89/00918
FILING DATE: 25-JAN-1989
ATTORNEY/AGENT INFORMATION:
NAME: Fleit, Martin; Gollin, Michael A.
REGISTRATION NUMBER: 16,900; 31,957
REFERENCE/DOCKET NUMBER: 47078-042
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 789-3400
TELEFAX: (202) 789-1158
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 408 residues
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: polypeptide
US-08-450-962-5
Query Match 12.4%; Score 230.5; DB 3; Length 408;
Best Local Similarity 24.9%; Pred. No. 3.5e-12;
Matches 93; Conservative 61; Mismatches 154; Indels 65; Gaps 14;
QY 3 PGEALLAGLLVMVLAVALLS-----NALVLLCCAYSAELRTRASGVLLVNLGLHLLAAL 58
DB 34 PWEAALAGAL---LALAVLATVGGNLLVIVAIATWTPRLQT-MTNVFTSLAAADLVMGLL 89
QY 59 DMPFTLLGVNMGRTSPAGCQVIGFLDTFLASNAALSVAALSADOMLAVGFLRYAGRL 118
DB 90 VVPPAATLALTGHWPGLGATGCELWTSVDVLCVTSIETLCALAVDRYLAVTNPLRYGALV 149
QY 119 RPRVAGLLGCAGWSLAFSGAALGCSW--LGYSSAFASCSLRLPPEPRPFAAFTATL 176
DB 150 TKRCARTAVLVVWVSAVSPAPIMSQWVGVADAEARQCH-----SNPRCCAFASNM 202
QY 177 -----HAGFVLPLAVCLTSLQVHRVARHC-----QRMDTVTMKALA--- 215
DB 203 PYVLLSSVSFYLLVMLFVYARVFWATQRLRLGELGRFPPEESPAPSRSLAPAP 262
QY 216 ----LLADLHPSVRQCLTQKRRHRATKIGIAIATFLICFAPYVMTL-----AEL 265
DB 263 VGTCAPEGVACGRPARLLPLREHRLCTGLINGTFLCWLFFFLANVLALGGPSL 322
QY 266 VP---FVTNAGWILSKCLTYSKAVADPFTYSL---LRRPFRQVLAVGWHRLKRTPRP 319
DB 323 VPGPAFLALN--W-----LGYANSAFNPLIYCRSPDFRSAPFRLLRCGRRL---PPEP 371
QY 320 ASTHDSLDVAGM 332
DB 372 CAARPALEPESGV 384
RESULT 13
US-08-448-631-2
Sequence 2, Application US/08848631
Patent No. 6635442
GENERAL INFORMATION:
APPLICANT: EMORINE, Laurent; MARULLO, Stefano;
APPLICANT: STROBERG, Donny
TITLE OF INVENTION: INTRON/EXON OF THE HUMAN AND
TITLE OF INVENTION: MOUSE a3-ADRENERGIC RECEPTOR
GENES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: KECK, MAHIN & CATE
STREET: P.O. BOX 06110
CITY: CHICAGO
STATE: ILLINOIS
COUNTRY: U.S.A.

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; ZIP: 60506-0110
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3-1/2" diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: ASCII
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/848,631
; FILING DATE: 08-Jun-1999
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/721,571
; FILING DATE: 25-MAY-1990
; APPLICATION NUMBER: PCT/FR89/00918
; FILING DATE: 25-JAN-1989
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Fleit, Martin; Gollin, Michael A.
; REGISTRATION NUMBER: 16,900; 31,957
; REFERENCE/DOCKET NUMBER: 47078-042
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 789-3400
; TELEFAX: (202) 789-1158
;
; INFORMATION FOR SEQ ID NO: 2:
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 408 residues
; TYPE: amino acid
; TOPOLOGY: linear
;
; MOLECULE TYPE: <Unknown>
; DESCRIPTION: Polypeptide
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
;
; US-08-848-631-2
;
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; Query Match 12.4%; Score 230.5; DB 4; Length 408;
; Best Local Similarity 24.9%; Pred. No. 3.5e-12;
; Matches 93; Conservative 61; Mismatches 154; Indels 65; Gaps 14;
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; QY 3 PGEALLAGLLVWVLAVALLS-----NALVLLCCAYSAELELTRASGVLLVNLGLHLLLAAL 58
; DB 34 PWEAALAGAL---LALAVLATVGGNLLVIVAIAWTPRLQT-MTNVFTVSLAAADLVMGILL 89
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; QY 59 DMPEFTLLGWMGRGPSAPGACOVIGFTDTFLSNAALSVAAALSADQWLAVGPPLEAYAGRL 118
; DB 90 VVPPRAATIALGHVPLGATGELWTSVDVLCVTASLETICALAVDEYLAVTNPLRYGALV 149
;
; QY 119 PRYAGLLGCAGQSLAFSGAALGCSW---LGYSSAFASCURLPEPPERPRFAAFTATL 176
; DB 150 TKRCARTAVLWVVVSAVSPAPIMSQWVRVGADABAQRCH-----SNPRCCAFASNM 202
;
; QY 177 -----HAGVFVLPLAVLCLTSLQHVARRHC-----QMDTVMTKALA--- 215
; DB 203 PVLVLSSVSFYLPLVWLVFVAVFVAVTRQRLRUGELGRPPPESPAPSRSLAPAP 262
;
; QY 216 ----LLADLHPSVRQCLIQKRRRHRATRKIGIAIATFLICFAPVWMTL-----AEL 265
; DB 263 VGTCAPEGVGPACGRRRPARLLPLREHEALCTGLINGTFTLCWLPPFLANVLRALGGPSL 322
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; QY 266 VP---FVTNNQWGLSKCLTYSKAVADPTYSL---LRPPRQVLAGWVHLLKRTTRP 319
; DB 323 VEGPAFLAIN--W-----LGYANSAFNPLIYCRSPDFRSAPARLLCRCGRRL---PPEP 371
;
; QY 320 ASTHDSLLDVAGM 332
; DB 372 CAARAPALPPSGV 384
;
;
; RESULT 14
; US-08-848-631-5
; Sequence 5, Application US/08848631
; Patent No, 6635442
;
; GENERAL INFORMATION:
; APPLICANT: EMORINE, Laurent; MARULLO, Stefano;
; STROSBURG, Donny
;
; TITLE OF INVENTION: INTRON/EXON OF THE HUMAN AND
; MOUSE a3-ADRENERGIC RECEPTOR

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US-09-479-128-2
; Sequence 2, Application US/09479128
; Patent No. 6319710
; GENERAL INFORMATION:
; APPLICANT: Berglind Ran Olafsdottir
; APPLICANT: Jeffrey Gulcher
; TITLE OF INVENTION: HUMAN NARCOLEPSY GENE
; FILE REFERENCE: 2345.1005-001
; CURRENT APPLICATION NUMBER: US/09/479,128
; CURRENT FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/379,083
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-479-128-2

Query Match 12.4%; Score 230.5; DB 4; Length 425;
Best Local Similarity 25.3%; Pred. No. 3.7e-12;
Matches 94; Conservative 55; Mismatches 154; Indels 69; Gaps 13;

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QY	65	LGVMEGRTPSAPGACQVIGFLDTFLASNAALSVAAASADQMLAVGFFPLRYAGRIRPRVAG	124
DB	105	LVDITESMLFGHALCKVIPYLOAVSVAVLTSLFIALDRWYAIChPLLFKSTAR-RARG	163
QY	125	LLLGCAWGCSLAFSGAALGCSWLGYSAPASCSLRLPPEPRPFAA-----FTA	174
DB	164	SLIG-IWAVSLAI-----WVQAAVMGCSVLPELANRTRLFVCDERWADDLYPK	213
QY	175	TLHAVGVFLP-LAVLCLTSLOVHRVARHCQRMDDVTVMKALA-----LLADL-----	220
DB	214	IYHSCFFIVTYLAPLGLMAMAYFQIFRXLWGRIQPGTTLSALVRNWKRPDQGLDLEQGLS	273
QY	221	-HPSVRQRCI-----IQKRRHRHATRKIGIATATLICFAP-----YVMTFLA----	263
DB	274	GEFQPRARAFLEAVKQMRARRKAKMLMVLLLVFALCYLPISVLNVLKRVFGMFRQASDR	333
QY	264	ELVPFVTVNAQWGLSKCLITYSKAVADPFTYSLLRPRPQVIL-----AGMVHRL	313
DB	334	EAVYACFTFSHW-----LVYANSAANPIIYNFLSGKREQKAFSCCLPLGCPGSLK	387
QY	314	KTPRPASTHDS	325
DB	388	APSPRSSASHKS	399

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Job time : 24 secs